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AUTHORS
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18036.975 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-		Description	AY398790 Homo sapi	AY398792 Mus muscu	AY398791 Pan trogl	AK080686 Mus muscu
SUMMARIES			AY398790	AY398792	AY398791	AK080686
		DB		53	5	디
•		Match Length DB	3371	3371	3273	4109
	* Query	Match	59.2	43.6	42.3	26.5
		Score	3369.4 59.2 3371	2486.2	2408.8	1510.8
	Result	No.		7	'n	4

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

gene trios Science 302 (5652), 1960-1963 (2003) 146/1302

PUBMED REFERENCE AUTHORS

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A	AUTHORS	Clark	, A.G.,	Glanow	gki.	S., Nielson, R., Thom	P., Kejari	1, A.,
		Todd, M.A.,	M.A.,	Tanenbaum, D.M.,	E,	D.M., Civello, D.R., Lu, F	., Murph	
		Adams	M.D.	and Car	; ; ;	Zneng, A.H., White, I.	Sulusky, u	:
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment by sequencing genomic exons and ordering
them based on alignment by sequencing genomic exons and ordering
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/mol_type="genomic DNA"
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/ib_xref="taxon:9606"
/locus_tag="HCM0008"
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qq	21 igracciecaagaaarrraaaaccarrieccaccaaarcacceee	108
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Ор	81 GCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCCTGCCTCCAC	114
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ò	ACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCA	CGGCGGCTGG 1451
ΩĐ	61 CAC	crec 132
ò	52 AGCCACTGGTCACCTTGGTCTTCATGCTCTGTGACTGTGG	ACGC 151
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ò	1512 ATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGGGAAGAATTGCA	TGGC 157
d d	81 AT	riddc 144
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ò	1632 TCCCCGTGGTCGCCTGCACTGTCACCTGTGCCGGTGGGATCCGGAGACC	3GTC 16
ДQ	1501 TCCCGTGGTCGGCCTGCACTGTCTGTCCGGTGGATCCGGGAGC	ddrc 156
ò	1692 IGCAACAGCCCIGAGCCICAGTACGGAGGAAAGGCCIGCGIGGGGAAG	GCGT 175
qq	1561 TGCAACAGCCCTGAGCTCAGTACGGAGGGAAGGCCTGCGTGGGGATG	GCGT 162
ò	1752 CAGATGTGCAACAAGAGGAGCTGCCCCGTGGATGGCTGTTTATCCAACCCCTGCTT	1
Ор	71 C3	cccc 168
ò	1812 GGAGCCCAGTGCAGCAGCTTCCCCGATGGGTCCTGGTCATGCGGCTCCTV	CCTGTGGGC
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ò	2 TICITGGGCAATGGCACCCACTGTGAGGACCTGGACGAGTGTGCCCTGG	CCGACATC 19
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Analysis of the mouse transcriptome based on functional annotation
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

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Fax:81-45-503-9216)
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Encyclopedia Project of Genome Exploration Research in Riken contributed to
prepare mouse tissues
Encyclopedia Project of Genome Exploration Research in Riken Contributed to
prepare mouse tissues

Location, Qualifiers

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Mus musculus 10 days neonate cortex CDNA, KIKEN full-length
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning

REFERENCE AUTHORS TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKRN), inboratory for Genome Exploration Research Group, RIKEN), incorporation Research Group, RIKEN Genomic Sciences Center (SCC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:Genome-res@gsc.riken.go.]p, PRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                      (2002)
of 60,770 full-length
Nature 420, 563-573 (2
6 (bases 1 to 3530)
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3297 CGGGCCTATGGCTACTCCGGCGTGTCCCTCAAGGTGGTGAACTCCACCACCACGGGACGGGC 3356
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(base, 1912)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.U., F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                        GAGCACCTGCGGAATGCACTGTGGCACACAGGAAACACCCCTGGCCAGGTGCGCCACCTG
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Pred. No. 1.2e-193;
0; Mismatches 1243; Indels 114;
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/organism="Homo sapiens"
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                       GACCTGGACGCCTGGCCCAACCTCAATCTGGTCTGCGCCAACGCCAACGCCACTACCACTGC
                                                                  2125 GACCTGGACGGCTGGCCTAATGAAAACCTGGTGTGTGTGGCCAACGCAACCTACCACTGC
                                                                                                              2277 ATCAAGGATAACTGCCCCCATCTGCCAAATTCTGGGCAGGAAGACTTTGACAAGGACGGG
                                                                                                                                                                                                                                         2005 ATTGGCGATGCCTGCGATGATGACGATGACAAGATCCCCCGATGACAGGGACAAC
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3154 ACAGGAAACACCCCTGGCCAGCTGCCCTGTGGCATGACCTCGTCACATAGGCTGG 3213 3444 AAGGACTACACGCCTATAGGTGGCACCTGTCACACGCCTACATCAGA 3503 3214 AAAGATTCACCGCCTACAGATGGCTCTCAGCCCCAAAGACGGGTTCATTAGA 3273 3214 AAAGATTCACCGCCTACAGATGGCTCTCAGCCCCAAAGACGGGTTTCATTAGA 3273 3504 GTCTTAGTGCATGAAGAAACAGGTCATGGCAACTCAGGACCTATCTAT	AY4 ON Mus GES GSS Mus SM Mus	tia; Nie] Nie] Nie] Iutior 1963	AUTHORS CLAIK, A.G., Glanowski, S., Nielson, K., Thomas, P., Kejariwai, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Int. F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  TILLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, GOURNAL This sequence was made by sequencing genomic exons and ordering The based on alignment.  ATURES 1.3240  ACORDINES 1.3240  ACOR	ene Local Si hes 2071; hes 2071; and 270 G 270 G 84 G 330 A 390 A
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	2604 GACACGGATGGTGGGGGGATCACTGTGACAACTGCCCCCTGGTGCACAACCCT 2663		2864 GAIGATGGCTGAAAAGATGATTTGACCATGACAGTGTGCCAAACATC 2733 2964 GAIGATGTGTGTCCTGAAACAATGCCATCAGTGACCATCAGGAACTTCCAGATG 3023 294 GAIGACATCTGTCCTGAAAACAATGCCATCAGTGACGATTCCAGATG 3023 3024 GATGACATCTGTCCTGAAAGAACACCCAAATGATCCAACTGGGTCATTCGCCATTCCAGTG 2793 3024 GATGACATCTGGAACCCCAAAAGGAACACCCAAAATGATCCAACTGGGTCATTGGCCATCAA 3083 1084 GGCAAGGAGCTCGAAAGGAACACCCGAAAATGACCCTAACTGGGTTGTTACGCCATCAG 2853 3084 GGCAAGGAGCTCGTTCAGACAGCCAACTCGGACCCCGGCATTGACGGGTTTTGACGAG 3143 1	3144 TTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAACACTGACGGACG

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Best Local Similarity 97.6%; Pred. No. 9.1e-118;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B. NIH-MGC http://mgo.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llhi.gov

littp://image.llhi.gov

Location/Qualifiers

Location/Qualifiers AGENCOURT 8744271 Lupski sciatic\_nerve Homo sapiens cDNA clone IMAGE:6205936 5', mRNA sequence.
BQ933301.1 GI:22348684
EST. 4825 ŝ 4885 5004 179 AGAATACATAGAGAATAATGAGGAGTTTATGATGAACCTT-AATATATAATGTTGCCAG CAAACGCTGAAAA -GAATCAGCATTTAGTCTTGCCAGGCACACCCAATAATCAGTCATGT 4766 TGAAAATATGAGGCTTGATAATATTAGGTTGTCACGATGAAGCATGCTAGAAGCTGTAAC TGAAAATATGAGGCTTGATAATATTTAGGTTGTCACGATGAAGGCATGCTAGAAGCTGTAAC CGATTTTAGTTCAATATTTGTTTACTGTTATCTATCTGTGTATATGGAATTCTTTTAATT CTAGTAACACATATGTAGTATTATTTCTAGAAACAACATCTAATAAGTATATAATCCTG CGATTITAGITCAATATTIGITACTGITATCTATCTGCTGTATATGGAATTCTTTAATT Gaps . 9 Length 939 Indels

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5'-TCGACCACGCGTCCG-3' and
5'-TCGACCACGGCGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies."
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                                                       organism="Homo sapiens"
                                                                         /mol_type="mRNA"
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ity sequence stop: (
Location/Qualifiers
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Homo sapiens (human)

Homo sapiens

ENKaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

In (bases 1 to 891)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-remail.nih.gov,

Contact: Robert Strauberg,

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://imaga.llh.gov.

Plate: LiAM13614 row: i column: 07
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

To (Dases 1 to 778)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP istitute, Cancer Genome Anatomy Project (CGAP), Thuror Gene Index

Tumor Gene Index

Tumor Gene Index

Thore Tages Frausberg, Ph.D.

Email: Cagapbs-refmail.nih.gov

Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of Orthoapedics

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this CDNA.
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UI-H-EZO-bar-m-21-0-UI 3', mRNA sequence.
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Genoscope - Centre National de Sequencage
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BP 192 191006 EVRY cedex - France
BP 193 191006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filangalifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG0072F12_CS00670_1.
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1 (bases 1 to 896)

1 in, N.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                           -CCTGTGAAAATATGAGGCTTGATAATATTAGGTTGTCACGATGAGGCATGCTAGAAGCT
                                                                  721 CCCTGTGAAAATATGACGCTTGATAATATTAGGTTGTCACGATGAAGCATGCTAGAAGCT
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763 bp mRNA linear EST 26-NOV-2003
MACCOURT 16368996 NIH MGC_220 Homo sapiens CDNA clone
CK000113
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                                                                                                              5304 TTGTTTTGCTGCACTTTTTACTTTTTTGCGTGTGGAGCTGTATTCCCGAGACCAACGAAG
178 ACACATTGCATTTTGATAAAATTAATTTTGTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTG 119
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Pred. No. 1.2e-102;
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Homo sapiens
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                                                                                                                                                         /day stage="Adult"
//day stage="Adult"
//day stage="Adult"
//dab_host="DH10B (Life Technologies)"
//dlob_host="DH10B (Life Technologies)"
//dlob="DH10B (Life Technologies)"
//dlob="Organ: Left Felvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: Left Felvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: Left Felvis; Vector: pT7T3-Pac (Pharmacia)
//dreft CGAP_CH1 is a cDNA library containing the following
tissue(s): Chondxosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecok I
adaptor, diseated with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT) 18 tail. The sequence tag for this library is
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                                                                                  /organism="Homo sapiens"
/mol_type="mRNR,"
/db_xref="taxon:9606"
/clone="UT-H-EZO-bar-m-21-0-UI"
/tissue_type="Chondrosarcoma Grade II"
                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E20
TAG_SEQ=ATCTAATATG"
 sequence: 356-404, > (CAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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es 751; Conserv
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Best Local Si
Matches 751
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I (bases 1 to 937)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                      CCAGATGGTCCCCTTGGATCCCAAAGGGACCACCCAAATTGATCCCAACTGGGTCATTCG
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Tissue Procurement: Dr. James R. Lupski

ONNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM13621 row: i column: 13

High quality sequence stop: 613.

Location/Qualifiers

// organism="Homo sapiens"

// Mol_type="mRNA"

// Ab zere="Laxon:9606"

// Sex="maile"

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Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this CDNA
sequence: 637-685, >(CAAA)n#Simple_repeat
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UI-H-FH1-bfe-k-04-0-UI.s1 NCI CGAP_FH1 Homo sapiens CDNA clone
UI-H-FH1-bfe-k-04-0-UI 3', mRNA sequence.
BUG18192 GI:23284407
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                              CAACTGCCCTTACGTGCACAACCCTGCCCAGATCGACACAGACAACAATGGAGAGAGGGTGA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 904)

1. (bases 2 to 904)

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1. (contact: Robert Strausberg, Ph.D.

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Matches 747; Conservative
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23-SEP-2002

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Location/Qualifiers

1. .750

/ organism="Homo sapiens"
/ db_xref="taxon:9606"
/ (Clone="thi-bfe-k-04-0-UI"
/ tissue_type="meNa"
/ db_xref="taxon:9606"
/ (Clone="thi-bfe-k-04-0-UI"
/ tissue_type="cell_line"
/ dev_stage="Adult"
/ lab_host="mello" (Life Technologies)"
/ lab_host="mello" (Clone Technologies)
/ lab_h
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Best Local Similarity 99.5%; Pred. No. 4.7e-100;
Matches 738; Conservative 0; Mismatches 4; Indels 0;
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TAG_SEQ=AGAATCCGGC"
                                                                                  ocation/Qualifiers
Seg primer: M13 FORWARD POLYA=Yes.
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March 10, 2004, 08:38:17 ; Search time 4861.4 Seconds
(without alignments)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1938) 1 (bases 1 to 1938) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G. REFERENCE AUTHORS is the number of results predicted by chance to have a

HC012609
HOMO sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2, mRNA (cDNA clone MGC:13616 IMAGE:4281085),

RESULT 1 BC012609 LOCUS DEFINITION

BC012609.1 GI:15214955

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

ALIGNMENTS

503 121141

5013 219071 280912

A10503 Artificial A10503 Artificial A10128 H sapiens B 14024 Sequence 1 A31184 pDBP1 DNA I A2123 H sapiens B 114025 Sequence 3 A2123 H sapiens B 114025 Sequence 5 A20470 preA-PAI-2.
X16490 Mouse RNA E M24657 Human plasm AC072501 Homo sapi AC009802 Homo sapi AC072501 Homo sapi AC16741 Papio anu X6453 R norvegicu G06377 human srs M256027 Sequence A114673 Collemur AC16673 Collemur AC166593 Rattus no AC16593 Rattus no AF416673 Homonap BC05423 Senomap BC012609 Homo sapi 10864 Sequence 1 A10352 Artificial AR380643 Sequence 702685 Human place 700581 Human place 700591 Human place 700501 Human plasm AR380644 Sequence 703603 Human plasm A02514 Synthetic g A1605 Molecule wi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES RNPAI2AMR G06377 AR380644 HUMPA12A BC012609 % Query Match Length DB 20751 1246 1000.8 985.8 985.8 567 Result

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TGLELLESEITYDKLNKWTSKDKWAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFN
KGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGGPQFVADH
PFLFLIMHKITNCILFFGRFSSP"
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Anote="SERPIN; Region: SERine Proteinase Inhibitors"
/db_xref="CDD:smart00093"
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                                                                                                                                                                                                                                                                           CAATGGAGGAGCATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGG
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                                                                                                                                                                                        1 GAGGAGCATTGCCGTCAGACAGCAACTCAGAGATAACCAGAGAACAACCAGATTGAAA
                                                                                                                                                                                                                    18 GAGGAGCATTGCCCGTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAA
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: k Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4505594.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Strauberg, R. Direct Submission Direct Submission Nammalian Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20832-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Jessica Fahey, Ezin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Best Local Similarity 99.7%; Pred. No. 0;
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Direct Submission
Submitted (12-JUN-1987) Andrew C. Webb, Department of Biological
Sciences, Wellseley, Mellesley, Mellesley, Mellesley, Mellesley, Mellesley, Mellesley, Malesley, Manuce-LPS-stimulated monocytes; clone-spon-1214
PAI-2 is a member CC of the serine protease inhibitor (serpin)
superfamily. It inhibits urokinase-type plasminogen activator. The
monocyte derived PAI-1.
Location/Qualifiers
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Catarrhini, Hominidae, Homo.
                                           Webb, A.C., Collins, K.L., Snyder, S.E., Alexander, S.J., Rosenwasser, L.J., Eddy, R.L., Shows, T.B. and Auron, P.E. Human monocyte Arg-Serpin cDNA. Sequence, chromosomal assignment, and homology to plasminogen activator-inhibitor J. Exp. Med. 166 (1), 77-94 (1987)
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                                                                                    1. .1880
/gene="PAII"
32. .1279
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/note="plasminogen activator inhibitor type 2 precursor"
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/gene="PA11"
/product="plasminogen activator inhibitor type 2
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99.5%; Pred. No. 0;
tive 0; Mismatches
/organism="Homo sapie:
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="7q21.3-q22.1"
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Matches 1865; Conservative
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Db 1682 CATAATGAAGAATAAGTATCCCTCCATGCCTTCTATAATAATATCTGGAAAAA 1741  Cy 1774 CATTAAACAATAAGCAATATGTTATGTGCCTTTCTAGAAATACATAACATATA 1833  Db 1742 CATTAAACAATAGCCAAATATGTTATGTGCATTTCTAGAATACATAACAATATA 1833  Cy 1834 TGTCTGTATCTTATATGAATAGTTATGTGCATTTCTAGAATACATAACAACAACAACAA  Db 1802 TGTCTGTATCTTATATTGCAAGTATATAATAAATAAATAA	PARSECUTE AND SEQUENCE 1189 from patent US 6607879. https://doi.org/10/10/10/10/10/10/10/10/10/10/10/10/10/	
	814 AMTIGCCGATGTGGCCATGTTGGAGCTGGGAAAGTGAAAACCATGAAACCB   813 AAATTGCCGATGTGCCATGTTGGAGCTGGGAAAGTGAAACCATGAAACCATGAAACCB   813 AAATTGCCGATGTGCGACAGCTGGAGCTGCTGGAAATGTGAAACCATGACAACCB   814 AAATTGCCGATGTGCGCACAGCTGGAGCTGCTGAAATGTGAAACCATGCACCCC   815   817 CAACAGTGGACCAGCAAGAAAATGGCTGAAATGATGAAACCATGCACCCC   812   817 CAACAGTGGACCAGCAAGAAATGCTCAGAACCATGAGAACCATGCCCC   813   817 CAACAGTGGACCAGCAAGAACACCATGACACCATGAGAACACATGCATTCAGAAACACATGCACAGAGAAGAACATTCAGAAACACATGAGAACACATGAGAACACATGAGAACACATGAGAACACATGAAAATTCAGAAACACACAC	

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plasminogen activator inhibitor.

plasminogen activator inhibitor.

SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 1854)

Antalis,T.M., Clark,M.A., Barnes,T., Lehrbach,P.R., Devine,P.L., Cloning and expression of a cDNA coding for a human monocyte-derived plasminogen activator inhibitor

Droc. Natl. Acad. Sci. U.S.A. 85 (4), 985-989 (1988)

1 2257578
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Human plasminogen activator inhibitor mRNA, complete cds.
J03603
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Traft entry and printed copy of sequence for [1] kindly provided by T.M.Antalis, 01/19/88. Polyadenylation signals are located at positions 1432-1437, 1637-1642, 1678-1683 and 1741-1746.
1561 ACTITIACTITIGITATITATITATATAATGGTGAGTITITAAATTATTATACTG
                                                                                                                                                                                                          1621 CCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTAATTTCCTATCTAAT
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                                                                                         GCTAGAAAAAGATTAATTCCTGGGTCAAGACTCAAACCAAAGGCAAAATCCCAAACTTG
                                                                                                                                                                                                            AAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAATGGGCTTTATCCTTTCCGTGTA
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Similarity 99.8t, Pred. No. 0; Conservative 0, Manatches 4, Indels 0, Gaps Conservative 0, Manatches 4, Indels 0, Gaps Conservative 0, Manatches 0, Indels 0, Gaps Conservative 0, Manatches 0, Manatches					
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Location/Qualifiers

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Anol_type="unassigned RNA"

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## ALIGNMENTS

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ss; differential expression; adipose tissue; cytostatic; hypotensive; antiarteriosclerotic; antidiabetic; anorectic; gene therapy; peroxisome proliferator-activated receptor gamma; PpARgamma; diabetes mellitus; obesity; hypertension; atherosclerosis; breast cancer; prostate cancer; colon cancer; polycystic ovarian syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Then invention relates to a new combination comprising 55 cDNAs (ADA24485 -ADA24539) or their complements that are differentially regulated in an adipose sample. Also included are detecting differential expression of one or more cDNAs in a sample containing nucleic acids, screening several molecules or compounds to identify a ligand that specifically binds a cDNA, a vector comprising the cDNA, a host call containing the vector, producing a protein, screening several molecules or compounds, producing
                                                                                                                         Human cDNA differential expressed in adipose tissue, INCYTE063646CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New combination comprising several cDNAs, useful for preparing a composition for diagnosing or treating diabetes mellitus, obesity, hypertension, atherosclerosis, or cancer of the breast, prostate or colon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 39-40; 84pp; English.
                 BP.
                 ADA24501 standard; cDNA; 1897
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an antibody and the isolated antibody. The cDNAs comprise sequences which are upregulated or downregulated in response to peroxisome proliferator-activated receptor gamma (PPARgamma) agonist. The combination comprising several cDNAs is useful for preparing a composition for diagnosing or treating diabetes mellitus, obesity, hypertension, atherosclerosis, cancer of the breast, prostate or colon, or polycystic ovarian syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. Additionally and AAB77789 represent sequences used in the examplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SBQ ID NO:1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
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colorectal carcinoma; ss.
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Pred. No. 0;
0; Mismatches 5; Indels 0
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                                                                                  Human colon cancer antigen encoding cDNA SEQ ID NO:251
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Best Local Similarity 99.7%;
Matches 1899; Conservative
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                                       (first entry)
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03-NOV-1999;
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CTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCCTATTAA 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of plasmid pcD-1214 cDNA 1900 bp insert encoding human precursor plasminogen activator inhibitor (PAI-2).
                                                                                                                                                                                                                                                                                                  TGCATTICTAGAAATACATAACACATATATATGTCTGTATGTTATATTCCAATTGCAAGTA
                                                                                                                                                                                               CTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACACCCTATTAA
                                                                                                                 TITATAACATTAACTTTTACTTTGTTATTTATTTATATAATGGTGAGTTTTTAAAT
                                                                                                                                                               TATTGCTCACTGCCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTAAT
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                                       CCAAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGAACAACTTCTGCTACCA
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Human precursor plasminogen activator inhibitor (PAI-2) having specified amino acid sequence and human mature PAI2 (23(5) to 415(P)) sequences are claimed. Fure DNA coding for human precursor PAI-2 and human mature PAI-2, a transfer vector pcD1214 as available in E. coli HB101 (pcD1214) (NRRL B-18161), transformed host cells (mammalian and yeast), and a method of culturing the transformed calls to produce PAI-2 are claimed. PAI-2 may have utility as a substitute for epsilon-aminocaproic acid (epsilon-ACA). The PAI-2 gene can be used as a probe to locate the gene coding for a PAI-2 or PAI-2-like activity. The PAI-2 can also be used to produce antibodies used in diagnostic assays. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 CABARGCARGCCCACCAGARCCTCTTCCTCTCCCCATGGAGCATCTCGTCCATGG
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                                                                                                                                                                                                                                                                                                                                                                                         Human precursor and mature plasminogen activator inhibitor - obtd. by recombinant techniques from lipo-polysaccharide-stimulated human monocytes.
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98.8%; Score 1886; DB 1; Length 1920;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1920 BP; 612 A; 393 C; 380 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       (NEME-) NEW ENGLAND MEDICAL CENT INC. (WELL-) WELLESLEY COLLEGE. (MASI ) MIT.
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P-PSDB; AAP80473.
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311 GGTTCATGCAGCAGATCCAGAAGGGTAGTTATCCTGATGCGATTTTGCAGGCACAAGCTG 370 361 CAGATAAAATCCATTCATCCTTCCGCTCTCTCAGCTCTCCCAATCAAT	841   GAGATGTTAGCATGTTCTGATGAAATTGCCGATGTCCCCTGGCTTGG   900   851

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                                                                                                                           GATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAACTCAGATCC
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                                         CGTCTAAACTCGGCTCAGCGCACAGCTGTACAGATGATGTACTTGCGTGAAAAGCTAAAC
TACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAAATGGGCTTTATCCTTTC
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                                                                                                                     Deoxyribonucleic acid - encoding recombinant human plasminogen activator inhibitor, used for preventing conversion of plasminogen to plasmin.
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                                                                                                                                                                           The sequence was obtd. from the combined sequences of lambda PAI-75.1 lambda PAI75.15, both isolated from a placental cDNA library. A recombinant vector contg. the DNA can be used to express PAI-2 which inhibits the conversion of plasminogen to plasmin and is used as an anticoagulant. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                   TACATGGGCTCCAGGGGCAGCACCGAAGACCAGATGGCCCAAGGTGCTTCAGTTTAATGAA
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 13; Indels 0;
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                                                                                                                                                         English.
      87US-00097482
                            (UNIW ) UNIV WASHINGTON (MONS ) MONSANTO CO.
                                                                                                                                                        Claim 1; Fig 4; 23pp;
                                                                                     WPI; 1991-215146/29
P-PSDB; AAR13007.
                                                               Wun TC;
      15-SEP-1987;
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                                                    1861
                    TCTAGAAATACATAACACATATATATGTCTGTATCTTATATTCAATTGCAAGTATAAAT 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.
                                                                                                                                                                                                                                                                                                                                        human; disease state; cytostatic; antiinflammatory; ophthalmological; antiatteriosclerotic; vulnerary; gene therapy; hypoxia-regulated condition; tumourigenesis; angiogenesis; apoptosis; inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; intric coxide synthesis; cancer; lachaemic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing; gene; ds.
                                       TCTAGAAATACATAACATAACATATATATATGTCTGTATCTTATATTCAATTGCAAGTATATAAT
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                                                                                                         Human disease related protein DNA sequence SeqID158
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Pred. No. 0;
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05-OCT-2001; 2001GB-00024037.
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Location/Qualifiers 49. .1296 /\*tag= a

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Minactivin is produced by induced human monocytes, certain macrophages and transformed cells of monocytic lineage (see WO 86/01212). Using the AA sequence obtd. for peptides of minactivin, oligonucleotide probes can spatheasleed, (see AAN70467- AAN70473, and AAN71181-N71183). The specific oligonucleotide probe may be radiolabelled and then used to screen cDNA libraries to identify clones contg. all or part of the minactivin gene. (Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                         DNA sequence encoding minactivin - used for monitoring and treating tumours and chronic inflammation such as rheumatoid arthritis.
                                                                                                                                                                                          Antalis TM, Barnes TM, Clark MA, Devine PL,
                                                                                                                                                                                                                                                                        Claim 3, pp34-37; 76pp; English.
                                                                                                                                                               (BIOT-) BIOTECHN AUSTR PTY (AUSU ) AUSTR NAT UNIV.
                                                                                                                                                                                                               WPI; 1987-265615/38.
P-PSDB; AAP70300.
                                                                                                       13-MAR-1986;
17-MAR-1986;
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                                                                                        GTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAACAATGGAGGATCTT
                           Query Match

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1849; Conservative 0; Mismatches 5; Indels 0
Sequence 2409 BP; 743 A; 500 C; 508 G; 658 T; 0 U; 0 Other;
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Tumour location, tumour inhibition; chronic inflammation; rheumatoid arthritis; ss.

Homo sapiens

Sequence encoding human minactivin.

(revised)
(first entry)

25-MAR-2003 13-MAY-1991

AAN70474;

AAN70474 standard; cDNA; 2409

RESULT 6

OY 1575 ACTTTAC OY 1575 ACTTTAC DD 1561 ACTTTAC OY 1635 CCTATTY OY 1635 AAATGCCI OD 1681 AAATGCCI OY 1755 AATAAATI OY 1755 AATAAATI OY 1755 AATAAATI OY 1756 AATAAATI OY 1815 AATAAATI OY 1815 AATAAATI OY 1815 AATAAATI	RESULT 7 AAN91177 ID AAN91177 standarc XX AC AAN91177; XX XX XX XX DT 25-MAR-2003 (rep DT 10-WAR-2003 (rep DT 12-JUN-1989 (fil) XX XX XX DE Sequence encoding XX YX XX YY YY	XX  PF 09-JUL-1987; 8  RX 09-JUL-1987; 8  XX  EBEHW BEHRINGW  XX  TOY N, Lecander XX  WPI; 1989-024876  PF PSDB; AAP91160  XX  New DNA encoding PT expressed protein PT diagnostically.  XX  XX  Sequence encodes CC be produced usin CC in this way and CC in this way.
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 PAI at posns. 120 (Asn replacing Asp), 404 (Asn replacing Lys), and (Ser replacing Cys). In addition Profine at posn. 393 is encoded by instead of CCG. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                   5; Indels 60;
                                      Query Match
91.7%; Score 1750; DB 1; Length 2424;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1823; Conservative 0; Mismatches 5; Indels 60;
                            Sequence 2424 BP; 723 A; 516 C; 533 G; 652 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA sequence encoding plasminogen activator inhibitor type 2 - and derived proteins and antibodies, useful therapeutically and in diagnosis.
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                                    Sequence encoding plasminogen activator inhibitor type 2 (PAI2) in human placental cDNA clone lambda-plc 1.
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Pred. No. 0;
0; Mismatches 5; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Table 1 Page 5; 6pp; German.
                                                                                    Protease inhibitor; thrombolytic; ss
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1. .1086
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Best Local Similarity 99.7%;
Matches 1670; Conservative
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        (first entry)
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P-PSDB; AAP80058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A lambda gt11 cDNA library constructed from phorbol-12-myristate-13-acetate stimulated cells of the human monocyte-11ke historytic lymphoma cell line U937 was screened. (See AAQ10850 and AAQ1081 for the probe sequences). From the putative positive clones, one was selected (lambda gt11-186) which appeared to contain the entire PAI-2 coding region. The linsert was cloned in MiJmp19 to give pDBP1 and was sequenced. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                plasminogen activator inhibitor-2; PAI-2; inflammation treatment; cancer;
                         1441 AGCAGATGATCTGTTAATTTCCTAATAAATGCCTTTAATTGTTCTCATAATGAAGA
                                                       1561 AGGCAAATATATGTTATGTGCATTTCTAGAAATACATAACACATATATGTCTGTATCT
                                                                               ATAAGTAGGTATCCCTCCATGCCCTTCTGTAATAAATATCTGGAAAAAACATTAAACAAT
                                                Query Match
73.7%; Score 1405.6; DB 2; Length 1412;
Best Local Similarity 99.7%; Pred. No. 3.1e-281;
Matches 1408; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1412 BP; 418 A; 311 C; 323 G; 360 T; 0 U; 0 Other;
                                                                                                                                                                                                   Encodes Plasminogen Activator Inhibitor-2
                                                                                                                                                                                                                                                         Location/Qualifiers
42. .1289
/*tag= a
/product= "PAI-2"
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89GB-00027480.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Steven J;
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P-PSDB; AAR10921.
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                                                                                                                                                       62 AATGGAGGATCTTTGTGTGGCAAACACTCTTTGCCCTCAATTTATTCAAGCATCTGGC
                                             Query Match
Best Local Similarity 95.3%; Pred. No. 1.3e-280;
Matches 1484; Conservative 0; Mismatches 4; Indels 69;
Sequence 1512 BP; 449 A; 318 C; 324 G; 421 T; 0 U;
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                                                                                                                                                                                                                                                                                                                             TATTTTTCGGCAGATTTTCCTCACCCTAAAACTAAGCGTGCTGCTTCTGCAAAAGATTTT 1320
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to treat inflammatory diseases e.g. rheumatoid arthritis, ulcerative
colitis and psoriasis and fibrinolytic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICTACATATITCIGCICITCIGAACAACTIC 1433
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/product= "PAI-2 variant"
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                                                                                                           The variant has amino acids 66-98 deleted. It retains the biological activity while lacking procease sensitivity of native PAI-2. The variant is pregd. by alteration of the DNA encoding PAI-2 and expression in hosts. DNA sequences encoding amino acids 66-98 were deleted from PAI-2 using the PCR technique of site-directed mutagenesis by overlap extension. See also AAQ11619. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 GCTAAACATTGGATACATAGAAGACCTAAAGGCTCAGATTCTAGAACTCCCATATGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                  62 AATGGAGGATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGGC
                                                                                                                                                                                                                                                                                                                                                           Gaps
Plasminogen activator inhibitor-2 variants with modified protease - to treat inflammatory diseases e.g. rheumatoid arthritis, ulcerative colitis and psoriasis and fibrinolytic diseases.
                                                                                                                                                                                                                                                                                                                                                           .66
                                                                                                                                                                                                                                                                                                                     Length 1482;
                                                                                                                                                                                                                                                                           Sequence 1482 BP; 438 A; 308 C; 320 G; 416 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                 Query Match
70.3%; Score 1341; DB 2; Length 1
Best Local Similarity 93.3%; Pred. No. 7.4e-268;
Matches 1453; Conservative 0; Mismatches 5; Indels
                                                                               Disclosure; Page 48-50; 88pp; English
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/*tag= b
/note= "synthetic-claim3"
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P-PSDB; AAR11352.
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AGAIGTTAGCAIGTTCTTGTTGCTTCCAGAIGAAATTGCCGATGTGTGCCACTGGCTTGGG
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                                                                                                                                             GCCTGAAGATGAAGTTGAGGTATACATACCCCCAGTTCAAATTAGAAGAGCATTATGAACT
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                                                    GCTGCTGGAAAGTGAAATAACCTATGACAAACTCAACAGTGGACCAGCAAAGACAAAAT
                                                                        1022 CAGATCCATTCTGAAAAGCATGGGCATGGAGGACGCCTTCAACAAGGGACGGGCCAATTT
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15. 1316
/*tag= a /product= "preB-PAI-2"
15. 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 cagaidanarccarrearcerredecrerereagereregearcarrecarecacadeda 429
                                                                                                                                                                                Addition of a signal sequence to PAI-2 not only facilitates secretion of the glycosylated 60 kb form of PAI-2 but also directs correct processing of the signal. The signal-contg. variant was constructed such that the artificial signal was fused to the NH2- terminal methiconine of PAI-2. Correct cellular processing of this signal peptide should result in a mature PAI-2 malecule of 41s amino acids with Net at its NH2-terminus. See AAQ11129 for PAI-2 with the alpha-1-antitrypsin signal sequence. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 ATTALTACTGGAAGTGTCATAAGCTGTTTTGGTGAGAAGTCTGCGAGCTTCCGGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GGTTCATGCAGCAGATCCAGAAGGTAGTTATCCTGATGCGATTTTGCAGGCACAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
Prepn. of glycosylated plasminogen activator inhibitor-2 (PAI-2) diagnosis and treatment of tumours, and in treatment of immuno:suppressant conditions and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.5%; Pred. No. 6.6e-249;
Matches 1253; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1328 BP; 377 A; 300 C; 317 G; 334 T; 0 U; 0 Other;
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120 129 180 240

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369 420

/label= alpha-1-antitrypsin

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AATGTGCAGAAGAAGCTAGAAAAAAGATTAATTCCTGGGTCAAGACTCAAACCAAAGGCA 609
                                                                                                                                                                                TGGCTGAAGATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAAC
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                                                                                                                                   ALCCTTTCCGTGTAAACTCGGCTCAGCGCACACCTGTACAGATGATGTACTTGCGTGAAA
                                                                                                                                                                 AGCTAAACATTGGATACATAGAACTAAAAGGCTCAGATTCTAGAACTCCCATATGCTG
                                                                                                                                                                                                                                      GAGATGTTAGCATGTTCTTGTTGCTTCCAGATGAAATTGCCGATGTGTCCACTGGCTTGG
                                                                                                                                                                                                                                                                AAATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGGTGA
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                                                                      ATGCTGTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAATGGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen activator inhibitor; PAI-2; signal sequence; diagnosis; treatment; tumour; inflammation; secretion; alpha-1-antitrypsin; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PreB-PAI-2 with alpha-1-antitrypsin signal sequence.
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(first entry)
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06-JUN-1991
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Location/Qualifiers
15. .1328
/\*tag= a
/product= "preB-PAI-2"
15. .86
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                                                                                                                                                                                                                                                                                             Addition of a signal sequence to PAI-2 not only facilitates secretion of the glycosylated 60 kD form of PAI-2 but also directs correct processing of the signal. The signal-contg. variant was constructed such that the human alph-1-antitrypsin signal was fused to PAI-2 without its NA2-terminal methionine. Correct cellular processing of this signal peptide should result in a mature PAI-2 molecule of 414 amino acids with Glu at its NA2-terminus. See AAQ11128 for PAI-2 with a synthetic signal sequence. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                    - for
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                                                                                                                                                                                                                 Prepn. of glycosylated plasminogen activator inhibitor-2 (PAI-2) diagnosis and treatment of tumours, and in treatment of immuno:suppressant conditions and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.4%; Pred. No. 1.5e-247;
Matches 1247; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1340 BP; 374 A; 307 C; 318 G; 341 T; 0 U; 0 Other;
                                                                                                                                                     Bunn CL;
                                                                                                                                                                                                                                                                        Disclosure; Fig 8; 70pp; English
                                                                          89AU-00006179
                                                                                                   89AU-00006179
                                                                                                                                                      Whitfeld P, Richardson MA,
                                                                                                                            (BIOT-) BIOTECHN AUST PTY
                                                                                                                                                                              WPI; 1991-102074/14.
P-PSDB; AAR11353.
                                                                          05-SEP-1989;
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                        WO9103556-A.
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GCAAAATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGG 657
                                                                                                                                                                                                              A PAI-2 positive clone was isolated after screening a library (see AAQ21117-8). A BgIII site was created at the 5' end of the gene to create amutation in the third position of the second codon. A AlfII site was created at the 3' end to create mutations in the third position of the last codon and in the first base of the stop codon. A clone derived from this procedure was designated pDBP2. Two linkers were ligated with the BgIII-AfIII PAI-2 gene fragment from pDBP2 into HindII + BAmHI digested minampl9 to form pDBP3. See also AAQ21117-19 and AAQ21121-25. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                     Antitumour molecules for treatment of neoplasms - comprises first region for binding to uPA receptor and second region for uPA inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 GGAATTATTTACTGGAAAGTGTCAATAAGCTGTTTGGTGAGAAGTCTGCGAAGCTTCCGGG
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                                                                                                                                                                                                                                                                                                                                        Sequence 1290 BP; 377 A; 289 C; 305 G; 319 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.2%; Pred. No. 2.2e-247;
Matches 1248; Conservative 0; Mismatches 10;
                                                                                                                                                                                           Disclosure; Fig 2; 57pp; English.
                     90GB-00017083
                                             90GB-00017083
                                                                                             Courtney MG;
                                                                      (DELZ ) DELTA BIOTECH
                                                                                                                    WPI; 1992-051155/07.
P-PSDB; AAR20797.
                                                                                             Ballance DJ,
                      03-AUG-1990;
                                               03-AUG-1990;
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                         CCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGGTGAAGGT
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25. .1272
/*tag= a
/label= PAI-2
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Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of

WPI; 2003-268322/26

Claim 1; Page 298; 455pp; English.

toxic restoxicity.

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The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of more human toxic response genes. to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also determining the presence of a toxic response to the agent. Also comparising one or more polymocleotides or homologues from the genes corresponding to the partial sequences given in ABZ82842 to ABZ8764, or their fragments of at least 20 mucleotides, or homologues creponse gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of calls or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating the test gene expression profile of toxic response gene after exposure to a known toxic pharmaceutical or industrial agent, comparing the test comparing the test profile of toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test comparing the test profile of the expression profile of comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for exposure to other known toxic compounds. The methods are useful for toxic response and determining toxic appearance or a cellular, organical system level. The arrays comprising the human genes are useful for toxic toxic pharmaceutical responses on a cellular, or exposure to expect toxic compounds and chemicals
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                    Query Match
Best Local Similarity 99.5%; Pred. No. 3.3e-200;
Matches 1017; Conservative 0; Mismatches 5; Indels 0.
Sequence 1024 BP; 313 A; 233 C; 234 G; 244 T; 0 U; 0 Other;
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Dunn RT, Adkins K,

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(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

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814 CTCAGAITCTAGAACTCCCATATGCTGGAGATGTTAGCATGTTCTTGTTGCTTCCAGAIG 873	۸
723 CTGTACAGATGATGTACTTGCGTGAAAAGCTAAAACATTGGATACATAGAAGACCTAAAGG 782	Д
754 CIGTACAGATGAACTTGCGTGAAAGCTAAACATTGGATACATAGAAGACCTAAAGG 813	¥
663 CATTIGAGAAGAAACTAAATGGGCTITATCCTTTCCGTGTAAACTCGGCTCAGCGCACAC 722	Д
694 CATTIGAGAAACTAAATGGGCTTTATCCTTTCCGTGTAAACTGGGCTCAGCGCACAC 753	*
603 ATGGGGATACCAGGATGGTCTGGTGAATGCTGTCTTCAAAGGAAAGTGAAAACTC 662	д
634 AIGGGGATACCAGGATGGTCCTGGTGAATGCTGTCTAATGGAAAGGAAAAAACTC 693	>
543 CCTGGGTCAAGGCTAAACCAAAAATCCCAAAACTTGTTACCTGAAGGTTCTGTAG 602	д
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Copyright (c) 1993 - 2004 Compugen Ltd.
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| Sequence 1188, Application US/09023655
| Patent No. 6607879
| GENERAL INFORMATION:
| APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Selhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLU TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES:
| AUTHOR OF SEQUENCES: 1508
| CORRESPONDENCE ADDRESS: 1508
| CORRESPONDENCE ALTO ALTO STREET: J14 PORTER DRIVE CITY: PALO ALTO COUNTY: USA ZIP: Word Perfect 6.1 for Windows/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS COMPUTER: HEREWITH US/09/023,655 FILING DATE: HEREWITH CLASIFICATION NUMBER: US/09/023,655 FILING DATE: PARCE OF THE CALLON NUMBER: US/09/023,655 FILING DATE: PARCE OF THE
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US-09-613-957-109
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US-09-21-107-109
US-09-643-597-111
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00
TELEPANICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1188:
SEQUENCE CHARACTERISTICS:
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GENERAL INPORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTY E PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
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                                      COUNTRY: USA

CONTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGERENCE/DOCKET NUMBER: 37,071
REGISTRATION NUMBER: 37,071
REGISTRATION INFORMATION:
TELEPHONE: (650) 855-0555
TELECOMOUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1189:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
STRANDENDESS: single
ILBARY: GENBANK
CLONE: GENBANK
CLONE: GENBANK
CLONE: GENBANK
CLONE: GESSISSES
LIBRARY: GENBANK
  PALO ALTO
CALIFORNIA
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                                                                                  AATAAATATCTGGAAAAACATTAAACAATAGGCAAATATATGTTATGTGCATTTCTAGA
                                                                                                                                                                                          Length 2409;
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOLDER, Jeffrey
APPLICANT: GOLDER, Jeffrey
APPLICANT: GOLDER, Jeffrey
APPLICANT: BARRES, Thomas M.
APPLICANT: BARRES, Neith H.
APPLICANT: GLARK, Michelle A.
APPLICANT: GLARK, Michelle A.
APPLICANT: LEHRBACH, Philip R.
TITLE OF INVENTION: MINACTIVIN
NUMBER OF SEQUENCES: 19
COMPUTER: Virginia
COUNTRY RABABBLE FORM:
MEDIUM TYPE: FOLOPY disk
COMPUTER: DASTEM: PC-DOS/MS-DOS
SOFTWARE: DASTEM: MUNDER: BAPLICATION UNDER: BAPLICATION NUMBER: BAPLICATION NUMBER: 16786/165 CHAC
TELEPHONE: (703)683-4109
TELEFAX: 899149
TELEFAX: 899149
TELEFAX: 899149
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MOLECULE TYPE: cDNA to genomic RNA
FEATURE:
                                                                                                                                                                                                                                                                            RESULT 3
WS-07-211-531-18
; Sequence 18, Application US/07911531
; Patent No. 5422090
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LOCATION: 49..1296
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LOCATION:
US-07-911-531-18
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                                         15 GTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAACAATGGAGGATCTT
                                                               1 GTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAACAATGGAGGATCTT
                                                                                                       Gaps
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               Indels
               4
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches
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         COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/693,636A
FILING DATE: 19910430
CLASSITCATION NUMBER: US 07/025,815
RILNG APPLICATION NUMBER: US 07/025,815
ATTORNEY/AGRYT INFORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 16786/155 CHAC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 836-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1847.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2409 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA to genomic RNA
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.8%;
Matches 1850; Conservative C
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APPLICANT: BARNES, Thomas M.
APPLICANT: BARNES, Thomas M.
APPLICANT: CLARK, Michelle A.
APPLICANT: CLARK, Michelle A.
APPLICANT: GOSS, Neil H.
APPLICANT: LEHRBACH, Philip R.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
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Sequence 18, Application US/07693636A
Parent No. 5426044
GENERAL INFORMATION:
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OY 1635 CCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTAATTTCCTATCTAAT 1694  Db 1621 CCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTAATTTCCTATCTAAT 1680  1695 AAATGCCTTTAATTGTTCTCATAATGAAGAATAAGTAAGT	RESULT 5 US-07-768-286B-1 ; Sequence 1, Application US/07768286B ; Patent No. 5444153 ; GENERAL INFORMATION: ; APPLICANT: GOSS, Neil H. ; APPLICANT: RICHARDSON, Michael A TITLE OF INVENTION: VARIANTS OF PAI-2	NUMBER OF SEQUENCES: 21  CORRESPONDENCE ADDRESS:  STREET: 1800 Diagonal Road, Suite 500  CITY: Alexandria  STATE: Virginia	COMPUTER READBALE PORM:  MEDIUM TYPE: Ploppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/07/768,286B	FILING DAIE: 19311011  CLASSIFICATION: 514  PRIOR APPLICATION DATA:  PILING DATE: 20-DEC-1990  ATTORNEY/AGENT INFORMATION:  NAME: BENT, Stephen A.  REGISTRATION NUMBER: 29,768	NPORMATION: 136-9300 136-9300 100: 1: 100: 1:	107 ACH	CELL TYPE: Monocyte CELL LINE: U937 INMEDIATE SOURCE: CLOSE: A 445 CLOSE: BTA 445 CHROMOSOME/SEGMENT: 18 MAP POSITION: 18q21-q23 FRAUTRE: NAME/KEY: CDS
	TACATAGAA           	915 GAATTAACCTATGACAAACTCAACAAGTGGACCAGCAAAGACAAAATGGCTGAAGATGAA 974 901 GAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGACAAATGGCTGAAGTGAA 901 GAAATAACCTATGACAACTCAACATGGACAAGACAAAGACCAAGATGAA 960 975 GTTGAGGTAACATAACAATTAAAATTAAAATATGAACTCAGATCCATTCTG 1034 961 GTTGAGGTATACAATACCCAGTTCAAATTAGAAGACATTATGAACTCAGATCCATTCTG 1034 961 GTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAACTCAGATCCATTCTG 1020	1035 AAAAGCATGGGCATGGAGGACGCCTTCAACAAGGGACGGGCCAATTCTCAGGGATGTCG 1094 1021 AGAAGCATGGACGCTTCAACAAGGGACGGCCCAATTTCTCAGGGATGTCG 1090 1095 GAGAGGATGACGTTCTTCTCAACAAGGGACGCATGGAAGATGACGTTCAACAAGGGACGCATGGAAGATGACTTCTTCTAACATGTTCAACATGATGAAGTTGAAGTTCAACATGAAGATGACCATGTTGAAGTTCAACATGTTCAACATGAAGATGACCATGAAGAAGAATGACCATTTCTTCTGAAGTTCCACCAAGCCATGGTGGAATGACAAGAATGACCATTTCTTCTGAAGTTCCACCAAGCCATGGTGGAATGTGAATGACATTACATTCTTTCT	1155 GAGGCACTGAAGCAGCCGCTGGCACAGGAGTGTTATGACAGGAGAACTGGACATGGA 1214	1275 TGCATTTTATTTTTGGGCAGATTTTGGTCACCCTAAAACTAAGGGTGCTGGTTCTGGAAA 1334		CTAAAATGGGATCATGCCCATTTAGATTTTTCCTTACTATCAGTTTATTTTTATAACATTA   CTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTATCAGTTTATTTTTATAACATTA   CTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTACTATTATATTTTTATAACATTA   ACTTTTACTTTGTTATTATTATTTATATAATGGTCAGTTTTTAAATTATTGCTCACTG

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J Sequence 3, Application US/07768286B

Patent No. 5444153

GENERAL INFORMATION:

APPLICANT: RICHARDSON, Michael A.

ITILE OF INVENTION: WAIANINS OF PAI-2

NUMBER OF SEQUENCES: 21

CORRESSED FOLDEY & Larder

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: 1800 Diagonal Road, Suite 500

CITY: Alexandria

CONPUTR: 10209

COMPUTR: 10209

COMPUTER: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/768,286B

FILING DATE: 20-DEC-1990

FILING DATE: 20-DEC-1990
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                                                                                       DB 1; Length 1610;
 LOCATION: 49..1296
OTHER INFORMATION: /product= "human plasminogen
OTHER INFORMATION: activator inhibitor type 2 protein"
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                                                                                     84.0%; Score 1602; Di
99.7%; Pred. No. 0;
:ive 0; Mismatches
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Best Local Similarity 99.73
Matches 1605; Conservative
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                       TGCTGTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAAATGGGCTTTA
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/157 CHAC
TELECOMMUNICATION INFORMATION:
TELEPAX: (703)836-9300
SEQUENCE CHARACTERISTICS:
TENDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CONA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CELL LINE: U937
INMEDIATE SOURCE:
CLONE: BTA 1916
FEATURE:

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122 AAAAGCAAGCCCCACCCAGAACCTCTTCCTCCCCATGGAGCATCTCGTCCACCATGGC 181
                                                                                                  GCTGCTGGAAAGTGAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGACAAAAT
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/function= "Product binds to
urokinase, tissue plasminogen activator"
/product= "PAI-2 variant, protease sensitive site
removed"
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//note= "Codes for human plasminogen activator
inhibitor type 2 protein in which amino acids 66
to 98 inclusive have been deleted."
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      Sequence 5, Application US/07768286B
Sequence 5, Application US/07768286B
Patent No. 5444153
GENERAL INFORMATION:
APPLICANT: GGOS, Neil H.
APPLICANT: RICHARDSON, Michael A.
TITLE OF INTURNION: VARIANTS OF FAI-2
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COMPUTR: 1900
COMPUTR: IBM PC compatible
COMPUTR: IBM PC compatible
COMPUTR: IBM PC compatible
COMPUTR: IBM PC COMPATION
SOFTWARE: DEATH RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
FILING DATE: 19911011
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 16786/157 CHAC
TELECOMMUNICATION INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 16786/157 CHAC
TELECOMMUNICATION INFORMATION:
NAME: BENY, Stephen A.
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)83-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.4%; Score 1342.6; Best Local Similarity 93.4%; Pred. No. 0; Matches 1454; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGHH: 1482 base pairs
TYPE: NUCLEIC ACID
STRANDEDNES: double
TOPOLOGY: Innar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENDE.
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL INE: Homocyte
CELL INE: NOBOCYTE
CELL LINE: NOBOCYTE
CELL LINE: NOBOCYTE
IMMEDIATE SOURCE:
CLONE: BTA 1922
FRATURE:
NAME/KEY: CDS
LOCATION: 22.1170
IDENTIFICATION METHOD: e
OTHER INFORMATION: /brc
OTHER INFORMATION: /brc
OTHER INFORMATION: /ev

OTHER INFORMATION: /ev

OTHER INFORMATION: /nc

OTHER INFORMATION: /nc
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
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HYPOTHETICAL: N
                       JS-07-768-286B-5
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                                        ACTABATABABACACAGABATAATTAGACAATTGTCTATTATAACATGACAACCCTATTA 1501
                                                                                TTTTATAACATTAACTTTTACTTTATTATTATTTATATATGGTGAGTTTTT 1618
                                                                                                                       TITIATAACATTAACTITIACTITGTIATITATTATTATTATAATAGGTGAGTITITT 1478
                    1322 CTGCTTCTGCAAAGATTTTTGTAGATGAGCTGTGTGCCTCAGAATTGCTATTTCAAATT
TAAGATAACCAAGTGCATTTTATTTTCGGCAGATTTTTGCTCACCCTAAAACTAAGCGTG
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MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
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LOCATION: 15.1319
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                                                               Length 1328;
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/product= "Synthetic signal peptide"
                                                             Query Match
Best Local Similarity 99.5%; Pred. No. 3.1e-293;
Matches 1253; Conservative 0; Mismatches 6;
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STREET: 1800 Diagount
CITY: Alexandria
CITY: Alexandria
COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DR PC COMPAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/679,052A
FILING DATE: 19910566
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION
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MOLECTLE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/07679052A
Sequence 16, Application US/07679052A
Patent No. 5298400
GENERAL INFORMATION:
APPLICANT: WHITFELD, Peter L.
APPLICANT: RICHARDSON, Michael A.
APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
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1800 Diagonal Road, Suite 500
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TELEFAX: (899149
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 1340 base pairs TYPE: NUCLEIC ACID STRANDENESS: double STRANDENESS: double characterists.
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LOCATION: 15..1331
FEATURE:
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                                                GAAGTGGGAGCCAATGCAGTTACCCCCATGACTCCAGAGAACTTTACCAGCTGTGGGTTC
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                           Gaps
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 Length 1340;
Score 1246; DB 1; Length 1
Pred. No. 2e-292;
0; Mismatches 5; Indels
Query Match
Best Local Similarity 99.6%;
Matches 1249; Conservative
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APPLICANT: Hu, Yi
APPLICANT: Ho. Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Nelke, D. Wade
TITLE OF INVENTION: NO. 6583269e1 Human Protease Inhibitor and Polynucleotides Encodi
FILE REFERENCE: LEX-0283-USA
CURRENT APPLICATION NUMBER: US/10/024,427
CURRENT APPLICATION NUMBER: US 60/256,287
PRIOR APPLICATION NUMBER: US 60/256,287
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Patent No. 6583269
GENERAL INFORMATION:
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Patent No. 6583269
GENERAL INFORMATION:
APPLICANT: Hu, Yi.
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 6583269el Human Protease Inhibitor and Polymuclectides EncodiFile Reference: LEX-0283-USA
CURRENT APPLICATION NUMBER: US/10/024,427
CURRENT APPLICATION NUMBER: US/026,287
FRIOR FILING DATE: 2001-12-18
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Pred. No. 4.4e-58;
0; Mismatches 565; Indels 30
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Similarity 53.6%;
18; Conservative
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ORGANISM: homo sapiens
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NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: COS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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STRANDEDNESS:
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LOCATION:
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STATE: MA
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                                                                                                                                                                Length 1278;
                                                                                                                                                                Query Match
14.4%; Score 274; DB 4; Length 12
Best Local Similarity 53.4%; Pred. No. 6.6e-57;
Matches 683; Conservative 0; Mismatches 565; Indels
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                               TYPE: DNA
ORGANISM: homo sapiens
IS-10-024-427-1
                                                             1278
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1021 GATATCTTTGAAAACGAGGGCTGATCTTACTGGAATCTCTCCAAGTCCCAATTTGTAC 1080
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901 AIGIGGCCTGGAGCGCAGCTCAGAAAACATGTCAGAAGAATCGGTGGTCCTTCCCC 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08315831A
Patent No. 5663299
GENERAL INFORMATION:
APPLICANT: Remodic-O'Donnell, Eileen
TITLE OF INVENTION: Human Monocyte Elastase Inhibitor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: September 30, 1994
CLASSIFICATION: 424
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US-08-662-318-12
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N
                                                                                                                                                                                                                                        DB 1; Length 1316;
                                                                                                                                                                                                                                Score 268.4; DB 1; Length
Pred. No. 1.5e-55;
0; Mismatches 436; Indels
OTHER INFORMATION: /codon_start= 49
                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.3%;
Matches 543; Conservative
                                                                         ) NAME/KEY: mat_peptide
) LOCATION: 49.1185
US-08-315-831A-12
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Sequence 12, Application US/08662318

Patent No. 5827672

GENERAL INFORMATION:

MUMBER OF SEQUENCES:

APPLICANT: Remold-O'Donnell, Eileen

TITLE OF INVENTION: Human Monocyte Elastase Inhibitor

NUMBER OF SEQUENCES:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: GOO Atlantic Ave.

GITY: Boston

STATE: MA

COUNTRY: Boston

STATE: MA

CONFUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CONFUTER: IBM PC compatible

OORHOTER: IBM PC compatible

OORHOTER: BADABLE FORM:

MEDIUM TYPE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/662,318

FILING DATE: September 30, 1994

ATTORNEY/ARCHITON NUMBER: 36,637

REFERENCE/DOCKET NUMBER: 36,637

REFERENCE/SOCKET NUMBER: 36,637

REFERENCE GIANTION NUMBER: 36,737

REFERENCE GIANTION NUMBER: 36,737

REFERENCE GIANTION NUMBER: 36,737

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REFERENCE GIANTI
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Best Local Similarity 55.3%; Pred. No. 1.5e-55;
Matches 543; Conservative 0; Mismatches 436; Indels
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NAME/KEY:
CDS
NAME/KEY:
OTHER INFORMATION: /codon_start= 49
1298 TIGCTCACCCTAAACTAAGCG 1319
                                                                    1176 Trcrrcccrragaagag 1197
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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LOCATION: 49.1185
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LOCATION: 49..1185
PCT-US95-12509-12
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HYPOTHETICAL: NO
ANTI SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapi
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                                                                                                        396 GGCCAGTGTGGATTTTCAGCATGCCTCTGAAGATGCAAGGAAGACCATAAACCAGTGGGT
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Human Monocyte Blastase Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: ADDRESSE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Ave.
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGCTCACCCTAAAACTAAGCG 1319
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14.1%; Score 268.4; DB 5; Length 1316;
Best Local Similarity 55.3%; Pred. No. 1.5e-55;
Matches 543; Conservative 0; Mismatches 436; Indels 3;
ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12509
FILING DATE: herewith
PRIOR APPLICATION NUMBER: 08/315,831
FILING DATE: 30 September 1994
ATTORNEY/AGENT INFORMATION:
NAME: PLUMER: 31 September 1994
ATTORNEY/AGENT INFORMATION:
NAME: PLUMER: 30 September 1994
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-3500
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LENGTH: 1316 Dase pairs
TYPE: nucleic acid
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Best Local Similarity 55.3%; Pred. No. 1.6e-55;
Matches 543; Conservative 0; Mismatches 436; Indels
TELECOMMUNICATION INFORMATION
                                                 TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 71(5)
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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CLONE: 334703
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US-09-016-434-710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATTAGAAGAGCATTATGAACTCAGATCCATTCTGAAAAGCATGGGCATGGAGGACGC 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACAGGAGGTGTTATGACAGGAGAACTGGACATGGAGGCCCACAGTTTGTGGCAGATCA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1056 CACAGCAGCATCGCAACTTTCTGCATGTTGATGCCCGAAGAAATTTCACTGCCGACCA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCGTTTCTTTTTCTTATTATGCATAAGATAACCAAGTGCATTTTATTTTCGGCAGATT 1297
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                                                                                                                                                                                                                                                                                                                                                                                                 TGCCGATGTGTCCACTGGCTTGGAGCTGCTGGAAAGTGAAATAACCTATGACAACTCAA 937
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                                                                                                                                                                                                                                                         696 GCTGGAACTGCCTTACCAAGGCGAGGTCAGCATGGTCATCCTGCTGCCGGATGACAT
       AATGATGTATCAGAAGAAAATTTGCATATGGCTACATCGAGGACCTTAAGTGCCGTGT
                                                                                                                                TCTAGAACTCCCATATGCTGGAGATG---TTAGCATGTTCTTGTTGCTTCCAGATGAAAT
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Parent No. 650038

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGCICACCCTAAAACTAAGCG 1319
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrcrrcccrragaagaaga 1197
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Search completed: March 11, 2004, 14:41:44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Appl
Sequence 17, Appl
                                                                                                                                                                                                                                March 11, 2004, 03:37:21 ; Search time 444.601 Seconds (without alignments) 15799.545 Million cell updates/sec
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1 gaggagcattgcccgtcaga......aacaaaaaataaaaaagg 1908
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1: /cgn2_6/ptodate/1/pubpna/PCT_NEW PUB.seq:*
2: /cgn2_6/ptodate/1/pubpna/DGO_NEW PUB.seq:*
3: /cgn2_6/ptodate/1/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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14 US-10-208-408-17
15 US-10-286-408-17
12 US-10-240-425-1566
12 US-0-262-812-82-89
1 US-09-813-388-178
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1 US-09-813-388-66
1 US-09-997-279-66
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Maximum Match 100%
Listing first 45 summaries
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Sequence 30504, A Sequence 1456, Appl Sequence 186, Appl Sequence 186, Appl Sequence 17, Appl Sequence 192, Appl Sequence 139, Appl Sequence 139, Appl Sequence 1075, Appl Sequence 1075, Appl Sequence 1075, Appl Sequence 1075, Appl Sequence 1084, Appl Sequence 188, Appl Sequence 188, Appl Sequence 338, Appl Sequence 109, Appl Sequence 
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; OTHER INFORMATION: Incyte ID No. US20030119009A1 063646CB1
US-10-084-817-27
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Sequence 27, Application US/10084817

Publication No. US20030119009A1

GENERAL INFORMATION:

APPLICANT: Susan Stuart

APPLICANT: Staron E. Plon

APPLICANT: Jacon M. Shohet

TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

CURRENT APPLICATION NUMBER: US/10/084,817

CURRENT FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-23

NUMBER OF SEQ ID NOS: 365

SEQ ID NO 27

LENGTH: 1908
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           14 US-10-029-386-14568

15 US-09-864-761-30504

16 US-09-813-318-186

17 US-09-813-358-186

18 US-09-813-358-186

19 US-09-823-187-1

10 US-09-823-187-1

10 US-09-823-187-1

11 US-10-10-28-937-279-186

12 US-10-98-94-247-192

13 US-10-10-136-133-1

14 US-10-10-136-135-1

15 US-10-10-136-1

16 US-09-925-301-368

17 US-10-10-136-1

18 US-10-084-817-148

19 US-09-928-301-368

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1908; Conservative 0; Mismatches
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TYPE: DNA ORGANISM: Homo sapiens
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Db 1201 GAACTGGACATGGAGGCCCACAGTTTGTGGCAGATCATCCGTTTCTTTTTCTTATTATGC 1260	Qy 1261 ATAAGAIAACCAAGTGCATTTTTTTTTCGCCAGATTTTGCTCACCCTAAAACTAAGCGT 1320 Db 1261 ATAAGATAACCAAGTGCATTTATTTTTCGCCAGATTTTGCTCACCCTAAAACTAAGCGT 1320	OY 1321 GCTGCTTCTGCAAAAGATTTTTGTAGACTGTGTGTGCCTCAGAATTGCTATTTCAAAT 1380	Qy 1381 IGCCAAAATTTAGAGAIGTTTTCTACATATTCTGCTCTTCTGAACAACTTCTGCTACC 1440 Db 1381 IGCCAAAAATTTAGAGAIGTTTCTACATATTTCTGCTCTTCTGAACAACTTCTGCTACC 1440	QY 1441 CACTAARAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCCTATT 1500 Db 1441 CACTAAATAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCCTATT 1500	Qy 1501 AATCATTTGGTCTTCTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTATCAGTTTA 1560  1501 AATCATTTGGTCTTCTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTATCAGTTTA 1560		Qy 1621 ATTATTGCTCACTGCCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTA 1680	-	4 4	TGTGCATTTCTAGAAATACATAACACATATATATGTCTGTATCTTATAN	Oy 1861 TATATAATAATAACCTGCTTCCAACAACAAAAAAAAAAA	RESULT 2 US-10-208-408-17 Sequence 17, Application US/10208408	GENERAL INFORMATION: APPLICANT: Schebye, Xiao Min TITLE OF INVENTION: TITLE OF DEPENDENCY: BENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR FITE DEPENDENCY: DA. 0048-1 115	FILE TAILCATION NUMBER: US/10/208,408 CURRENT FILING DATE: 2002-07-29 PRIOR APPLICATION NUMBER: 60/308,868	FALON FILING DATE: GUOI-0/-30   NUMBER OF SEQ ID NOS: 55   SOFTWARE: PERL Program   SEQ ID NO 17   FIRE PROGRAM	TYPE: DN   TYPE: DN   ORGANISM: Homo sapiens   FEATURE:	; NAME/KBY: misc feature ; OTHER INFORMATION: Incyte ID No. US20030096272A1 063646CB1 US-10-208-408-17	Query Match 99.4%; Score 1897; DB 14; Length 1897; Best Local Similarity 100.0%; Pred. No. 0;
121 CAAAAGCAAGCCCCACCAGAACCTCTCTCCCCATGGAGCATCTCGTCCACATGG 180	CCATGGTCTACATGGGCTCCAGGGGGAGCACCGAGGTGCCAGGGTGCTTCAGT 240	TTAATGAAGTGGGAGCCAATGCAGTTACCCCCATGACTTCAGAGAACTTTACCAGCTGTG 300	GGTTCATGCAGCCAATGCAATGCCCCCAAGAGCTCAAGAATTTACAAGCAAG	CAGATAAAATCCATTCATCCTCCGCTCTCTCAGATCAATCA	ATTATTTACTGGAAAGTGTCAATAAGCTGTTTGGTGAGAAGTCTGGGGAGCTTCGGGAAG 480	AATAINTICGACTCTGTCGGAATATTACTCCTCGGGCGCGGGGGGGGG	AATGTGCAGAAGAAGAAGAAAAAGATTAATTCCTGGGTCAAGATCCAAAGGCA 600	AAATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGCCTGGTGA 660	ATGCTGTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAACTAAATGGGCTTT 720 ATGCTGTCTACTTCAAAGGAAAACTCCATTTGAGAAAGAA	21 ATCCTTTCCGTGTAAACTCGGCTCAGCGCACACCTGTACAGATGAACTTGCGTGAAA 780 	840	841 GAGATGTTAGCATGTTCTTGTTGCTTCCAGATGAATTGCCGATGTGTCCACTGGCTTGG 900	901 AGCTGCTGGAAAGTGAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGAAGAAAAA 960 	961 TGGCTGAAGATGAAGTTGAGGTATACATACCCCGAGTTCAAATTAGAAGAGCATTATGAAC 1020 	1021 TCAGATCCATTCTGAAAAGCATGGGCATGGAGGACGCCTTCAACAAGGGACGGGCCAATT 1080 	1081 TCTCAGGGATGTCGGAGGAATGACCTGTTTCTTTCTGAAGTGTTCCACCAAGCCATGG 1140	1200	GGAACTGGGACGACGACGACGACTTGTGGCAGGACCACACGAGGGGGTTTTTTTT

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SEQ ID NO 261
LENGTH: 1935
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Wetzel, Uwe
APPLICANT: Wockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REPERENCE: 44921-502
CURRENT APPLICATION WUMBER: US/10/240,425
CURRENT APPLICATION NUMBER: DCT/US01/09847
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR APPLICATION NUMBER: PCT/US01/09347
PRIOR PILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER: OF SEQ ID NOS: 1588
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 1566
LENGTH: 1900
TUPLE TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1900;
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 Y00630
IS-10-240-425-1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

98.1%; Score 1872.6; DB 12; Lengt!
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 4; Indels
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ORGANISM: Homo sapiens
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Sequence 252, Application US/09962832
| Sequence 252, Application US/09962832
| Patent No. US20020110821A1
| GENERAL INFORMATION:
| GARBRAL INFORMATION:
| GARBRAL INFORMATION:
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatury TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatury TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatury TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatury FILIE OF INVENTION: US/60/235,077
| CURRENT FILIE DATE: 2000-09-25
| PRIOR PRILING DATE: 2000-09-25
| PRIOR PRILING DATE: 2000-09-25
| NUMBER OF SEQ ID NOS: 259
| SEQ ID NO 252
| INVENTION OF SEQ ID NOS: 259
| SEQ ID NO 252
| INVENTION OF SEQ ID NOS: 259
| SEQ ID NO 252
| INVENTION OF SEQ ID NOS: 259
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                     164474 TITTATAACATTAACITITACITITOITATTATTATTATTATAAAGGTGAGTTTTTAAA
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1442 ACTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCTATTA
                                                                                                                                     164534 Arcarrregrerreraaaregearcarecearrragarrrecerracrateaerrra
                                                                                                                                                                                       TITIATAACATTAACTTTTACTTTGTTATTTATTTATATAATGGTGAGTTTTTAAA
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Best Local Similarity 99.3%; Pred. No. 1.6e-213;
Matches 989; Conservative 0; Mismatches 7;
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; ORGANISM: Homo sapiens
US-09-962-832-252
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164654 GCCAAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGAACAACTTCTGCTACCT 164595
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Publication No. US20040043389A1
GENERAL INFORMATION:
APPLICANT: MCGATHY, Jeanette
APPLICANT: MCGATHY, Jeanette
TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases
TITLE OF INVENTION: and Disorders Associated Therewith
TITLE OF INVENTION: MAI-011
CURRENT APPLICATION NUMBER: US/10/235,192A
CURRENT FILING DATE: 2002-0-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45.
URNGHH. 191395
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                                                                                           | TGTGCATTTCTAGAAATACATAACACATATATATGTCTGTATCTTATATTCAATTGCAAG 1860
                                                                                                                                           TGTGCATTTCTAGAAATACATAACACATATATATGTCTGTATCTTATATTCAATTGCAAG 1869
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Best Local Similarity 99.3%; Pred. No. 1.8e-212;
Matches 990; Conservative 0; Mismatches 7; Indels 0; G
                                                                                                                                                                                       TYPE: DNA
; ORGANISM: Homo sapiens
US-10-235-192A-45
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1447 ATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCCTATTAATCAT 1506
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                                                                                 Query Match 29.4%; Score 560; DB 9; Length 566; Best Local Similarity 100.0%; Pred. No. 4.1e-117; Matches 560; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-813-358-178
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; ORGANISM: Homo sapien
US-09-997-279-178
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Patent No. US20020048759A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN AND ENDOMETRIAL CANCER
FILE REFERENCE: 210121.501
CURRENT APPLICATION NUMBER: US/09/813,358
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 222
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 178
LENGTH: 566
                       creagggargregagaggaargaccrerrrerrrergaggrerrecaccaagccarggr
                                                                     GGATGTGAATGAGGAGGGCACTGAAGCAGCCGCTGGCACAGGAGGTGTTATGACAGGGAG
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Sequence 178, Application US/09997279
Publication No. US20030059781A1
GENERAL INFORMATION:
APPLICANT: Chenault, Ruth A.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN AND ENDOWETRIAL CANCER
TITLE OF INVENTION: UNMERS: US/09/997,279
CURRENT APPLICATION UNMERS: US/09/997,279
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 230
SOFTWARES FRANCE: PARKED FOR Windows Version 4.0
SEQ ID NO 178
LENGTH: 566
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29.4%; Score 560; DB 10; Length 50
Best Local Similarity 100.0%; Pred. No. 4.1e-117;
Matches 560; Conservative 0; Mismatches 0; Indels
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                                            AGCCCCACCCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGCCATGGTC
                                                                                             TACATGGGCTCCAGGGCCAGCACCGAAGACCAGATGGCCAAGGTGCTTCAGTTTAATGAA
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Publication No. US20030059781A1

Publication No. US20030059781A1

Publication No. US20030059781A1

APPLICANT: Ku, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER

FILE REFERENCE: 210121.501C1

CURRENT FAPLICATION NOMBER: US/09/997,279

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 230

BENGTA: 503
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26.1%; Score 498.8; DB 10;
Best Local Similarity 99.6%; Pred. No. 3.2e-103;
Matches 500; Conservative 0; Mismatches 2;
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US-09-997-279-66
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Patent No. US20020048759A1

Patent No. US20020048759A1

APPLICANT: Eyle, Ruth
APPLICANT: Eyle, Ruth
APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: ADD DIAGNOSIS OF OVARIAN AND ENDOMBTRIAL CANCER
FILE REPERENCE: 210121.501

CURRENT APPLICATION NUMBER: US/09/813,358

CURRENT FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 222

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 66

LENGTH: 503

TYPE: DAM

ORGANISM: Home sapien
US-09-813-358-66
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Pred. No. 3.2e-103;
0; Mismatches 2; Indels 0
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Best Local Similarity 99.6
Matches 500; Conservative
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Sequence 13440, Application US/10029386
| Sequence 13440, Application US/10029386
| Sublication No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn. Sharron G. APPLICANT: Hanzel, David R. APPLICANT: Hanzel, David R. APPLICANT: Hanzel, David R. APPLICANT: Hanzel, David K. TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (FILE REPRENCE: AEDMICA-X-2 COURSENT PELICATION UNMERS: 0210/029,386 CURRENT PILING DATE: 2001-12-20 CURRENT PILING DATE: 2001-12-20 SOFTWARE ANDOMEX Sequence Listing Engine vere: 1.1 SEQ ID NO 13440
                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 TCAGATCCATTCTGAAAAGCATGGGCATGGAGGACGCCTTCAACAAGGGACGGGCCAATT 1080
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                                                                                                                                                                                                                  9; Length 482;
                        FEATURE:
OTHER INFORMATION: MAP TO AC009802.8
OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
US-09-864-761-13940
                                                                                                                                                                                                                                                                      Indels
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OTHER INFORMATION: MAP TO CHRIB.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.32
OTHER INFORMATION: WI HIT: M31551.1, BYALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P05120, EVALUE 1.00e-56
                                                                                                                                                                                                               Query Match

24.9%; Score 475.6; DB 9
Best Local Similarity 99.2%; Pred. No. 5.9e-98;
Matches 478; Conservative 0; Mismatches 4
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ORGANISM: Homo sapiens
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                                                                                                                                   428
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                                                                                                                                                                                                                                              CTGGAAAGTGTCAATAAGCTGTTTGGTGAGAAGTCTGCGAAGCTTCCGGGAAGAATATATT 488
                                                                                                                                                                                                                                                                      CTGGAAAGTGTCAATAAGCTGTTTGGTGAGAAGTCTGCGAGCTTCCGGGAAGAATATATT 481
                                                                                                                                Pacter: No. US200200487631

Batter: No. US20020487631

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTIVED FILE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTIVED FILE REFERENCE: Aconica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PLING DATE: 2000-02-04
FILE REFERENCE: Aconica-X-1
CURRENT PLING DATE: 2000-02-04
FILE REPERIOR FILE ON NUMBER: US/09/864,761
CURRENT PLING DATE: 2000-02-04
FRIOR APPLICATION NUMBER: US/09/30,366
FRIOR APPLICATION NUMBER: US/09/30,366
FRIOR APPLICATION NUMBER: US/09/30,366
FRIOR APPLICATION NUMBER: US/09/30/3066
FRIOR APPLICATION NUMBER: US/09/30/30/3066
FRIOR APPLICATION NUMBER: PCT/USO1/00666
FRIOR FILING DATE: 2001-01-30

                     CAGCAGATCCAGAAGGGTAGTTATCCTGATGCGAT
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US-10-27-632-122703/Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Identification and Mapping of Single Nucleotide
TITLE OF INVERTION: Identification and Mapping of Single Nucleotide
TITLE OF INVERTION: OF DAYAGE US OF 
                                                                                                                                                                                                                                                                                                                                                                                                   1022 CAGATCCATTCTGAAAAGCATGGACATGGAAGAAGGACGCCTTCAACAAGGGACGGGCCAATTT
                                                                                                                                                                                     902 GCTGCTGGAAAGTGAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGAAAT
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Pred. No. 3.4e-69;
0; Mismatches 3; Indels 0;
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                                                                            Query Match 20.3%; Score 387.6; DB 14; Length 596; Best Local Similarity 99.0%; Pred. No. 6.8e-79; Matches 390; Conservative 0; Mismatches 4, Indels 0;
; OTHER INFORMATION: EST_HUMAN HIT: BF666885.1, EVALUE 0.00e+00
US-10-029-386-13440
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Best Local Similarity 99.2%;
Matches 352; Conservative (
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; ORGANISM: Human
US-10-027-632-122703
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RESULT 14
US-10-029-386-27140
US-10-029-386-27140
Sequence 27140, Application US/10029386
Sequence 27140, Application US/10029386
Sequence 27140
Sequence Listing Engine vers. 1.1
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235 CAGATCCATTCTGAGAAGCATGGGCATGGAGGACGCCTTCAACAAGGGACGGGCCAATTT 176
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18.0%; Score 343.2; DB 14; Length 354;
Best Local Similarity 99.1%; Pred. No. 6.3e-68;
Matches 345; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA

CRGALISM: Homo sapiens

COTHER INFORMATION: EXPESSED IN LUNG, SIGNAL = 0.32

CTHER INFORMATION: EXPESSED IN LUNG, SIGNAL = 0.32

CTHER INFORMATION: EST HUMAN HIT: BF66685.1, EVALUE 0.00e+00

CTHER INFORMATION: NT HIT: M24657.1, EVALUE 0.00e+00

CTHER INFORMATION: SMISSPROT HIT: P05120, EVALUE 3.00e-47
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Sequence 865. Application US/10029386

Sequence 865. Application No. US20030194704A1

Sequence 865. Spilication No. US20030194704A1

SEQUENCE NOTE OF THE SET OF SET O
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247 GGATGTGAATGAGGAGGACTGAAGCAGCCGCTGGCACAGGAGGTGTTATGACAGGAGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 GCAGCTGGAAAGTGAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGACAAAAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 cadarccarrcrgagaagcardddcarddagacgccrrcaacaagdacgdccaarrr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GGATGTGAATGAGGAGGGCACTGAAGCAGCGGCTGCTGGCACAGGAGGTGTTATGACAGGAG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GGCTGAAGATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAACT
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17.7%; Score 337.2; DB 14; Length 544;
Best Local Similarity 99.1%; Pred. No. 1.9e-66;
Matches 339; Conservative 0; Mismatches 3; Indels 0;
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 0.86
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1248 bp DNA linear GSS 17-DEC-2003
Homo sapiens SERPINB2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Homo sapiens
Bukaryota, Materia, Chordata, Craniata, Vertebrata; Buteleostomi,
Bumalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 1248)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
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CA313606
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AUTHORS
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AY416314 Pan trog1
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AL574114 AL574114
                                                                                                                                                             March 10, 2004, 09:18:38; Search time 3158.9 Seconds (Without alignments) 18036.975 Million cell updates/sec
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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All Submitted (16.NOV-2003) Celera Genomics, 45 West Gude Ditve, Roceville, No. 2003, USA. Roceville, No. 2003, USA. Roceville, No. 2003, USA. Roceville, No. 2003, USA. Roceville, No. 2004, USA. Rocev	3 8 3 8 3 8		RESU. AY41. LOCUIDEFII DEFII ACCE. VERS: KEYW. SOUR(	REFE AU TI: JOI REFEBI	TI' JO' COMMI FEATI	ORIG Ou
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	AL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Driv Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ord them based on alignment.  Location/Qualifiers 1. 1248 /mol_type="genomic DNA" /mol_type="genomic DNA" /db_xref="taxon:9606" /mol_sign="SERPINB2" /locus_tag="HCM5849"	Match	ANTGAAGTGGGAGCCAATGCAGTTACCCCCATGACTCCAGGAACTTTACCAGCTGTGGG	TATTTACTGGAAAGTGTCAATAAGCTGTTTGGTGAGAAGTCTGCGGAGCTTCCGGGGAAGAA  [	ATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGGTACCAGGATGGTCCTGGTGAAT	CTAAACATTGGATACATAGAAGACCTAAAGGCTCAGATTCTAGAACTCCCATATGCTGGA 

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GCACAGGAGGTGTTATGACAGGGAGA 1202
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RESULT 3 AL550163 LOCUS LOCUS DEFINITION AL550163 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLOR AL550163 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA AL550163 2 GI:31271981 KEYWORDS RYMORDS Homo sapiens (human) ORGANISM Homo sapiens (human) ELKaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,		ng O	/ Organishm="mono saplens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1040YG06" /tissue_type="PLACENTA COT 25-NORWALIZED" /clone lib="Homo saplens PLACENTA COT 25-NORWALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer: Five prime and enriched, double-strand cDNA was primed, double-strand cDNA was directed with Not I and ECOR V	ORIGIN  Query Match  Best Local Similarity 98.2%; Pred. No. 3.7e-184;  Matches 1066; Conservative 7; Mismatches 9; Indels 3; Gaps 2;	QY         10 TGCCCGTCAGACAGCAACTCAGAGAATAACCAGAGAACCAGATTGAAACAATGGAGG 69	130 GCCCACCCAGAACCTCTTCCTCTCCCATGAGCATCTCGTCCACCATGGCCATGGTCTCTCTC	QY         250         TGGAGGCCAATGCGGTTACCCCATGACTTTACCAGGTTCAGGGTTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGGATAAAA         423
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Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Bukaryota, Metazoa, Chordates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1126)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12934006.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                      TGGAAAGTGTCAATAAGCTGTTTTGGTGAGAAGTCTGCGAGCTTCCGGGAAGAATATATTC 543
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/mol Lype="mRNA"
/mol Lype="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO40YG06"
/tissue type="PLACENTA COT 25-NORMALIZED"
/note="lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lit strand cDNA was primed with a Not1--oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer of the prime and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector, Library was normalized.
                                               For
                                                                                                                  Contact
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Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9202.f F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi-seq-cSoD1040BD03NP1&cluster=9202.f. Contac
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI040BD03NP1.
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53.9%; Score 1027.8; DB 9; Length 1126;
Best Local Similarity 98.1%; Pred. No. 1.3e-181;
Matches 1056; Conservative 13; Mismatches 5; Indels 3;
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Analysis of the mouse transcriptome based on functional annotation droug phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 1965)

Adachi, J., Alzawa, K., Akimura, T., Hara, A., Hashlzume, W., Hayasha, T., Hayasha, T., Hayasha, T., Hayasha, T., Hayasha, T., Hayasha, T., Imotani, K., Ishi, Y., Itoh, W., Kagawa, I., Kasukawa, T., Hayasha, T., Mori, P., Imotani, K., Ishi, Y., Itoh, W., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kalito, R., Saitoh, H., Kouda, M., Ohato, W., Nakamura, M., Nishi, K., Nomuyama, T., Numazaki, R., Murata, M., Nishi, K., Nomuyama, T., Numazaki, R., Murata, M., Saaki, C., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Saaaki, D., Saitoh, H., Saaki, K., Shiraki, T., Takahashi, P., Takaku-Akahira, S., Sano, H., Saaaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takaku-Akahira, S., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Nuramatsu, M., and Hayashizaki, Y., Vasunishi, A., Nuramatsu, M., and Hayashizaki, Y., Vasunishi, A., Nuramatsu, M., and Hayashizaki, Y. Dayar, T., Yasunishi, A., Naramatsu, M., and Hayashizaki, Y., Takahashi, P., Takaku-Akahira, S., Nuramatsu, M., and Hayashizaki, Y., Takahashi, P., Takaku-Akahira, S., Nuramatsu, M., and Hayashizaki, Y., Takahashi, P., Takaku-Akahira, S., Nuramatsu, M., and Hayashizaki, Y., Takahashi, P., Takaku-Akahira, S., Nuramatsu, M., and Hayashizaki, Y., Takahashi, P., Takaku-Akahira, S., Takaku-Akahira, S., Takaku-Akahira, S., Submitted (16-APP-2002) Yoshihide Hayashizaki, The Institute of Bryologua Toroup, A., Takaku-Akahira, S., Shirasyawa 230-0045, Japan (E-mail: genome-resogac. riken.go.jp/, Tel:81-45-503-9226,

Tax:81-45-503-9216,

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Blease visit our web site for further details.

URL:http://fantom.goc.riken.go.jp/,

10RL:http://fantom.goc.riken.go.jp/.
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/clone="c130020L09"
/tissue type="head"
/clone_Tib="RIKEN full-length enriched mouse cDNA library"
and the RIKEN Genome Exploration Research
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Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30020L09 product:serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2, full insert sequence. AKO81487.1 GI:26349182

HTC: CAP trapper.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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    TCTGCTCTTCTGAACMACYTCYGCTACCCACTAAATAAAAACACAGAAATAATTAGACAA
                                                                                                                          394 ITGTCTATTATAACATGACAACCCTATTAATCATTTGGTCKTCTAAAATGGGRTCATGCC
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Mach. Enzymol. 303, 19-44 (1999)
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(CB-0035 WEHL-3 DONA, RIKEN full-length enriched
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52.5%; Score 1000.8; DB 11; Lengt
Best Local Similarity 73.0%; Pred. No. 1.2e-176;
Matches 1366; Conservative 0; Mismatches 477; Indels
                                       (ovalbumin), member 2 (MGD|MGI:97609,
evidence: BLASIN, 100%, match=1899)"
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/note="putative"
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L. Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Yokohama Institute; 1.7-22 Suchiro-cho, Tsurumi, ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-resegeoriken.go.jp, Takaki, T., Takaku, T., Takaku
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374
                                                                                                                                                                                                                                Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Mateumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Ohaca,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Mateuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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/db_xref="MGI:2428955"
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/clasue_type="blood"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1952)
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/.

URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers
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/mol_type="mRNA"
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On Feb 16, 2001 this sequence version replaced gi:12944080.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
BRail: seqref@genoscope.ons.fr, Web: www.genoscope.ons.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9202.f For more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSODH002CE03NPl&cluster=9202.f. Contact:
Feng Liang Enail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODH002CE03NPl.
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/db_txef="taxon:9606"
/dboe="CS0DH0022405"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/clone="CS0DH002405"
/clone="Jihe="URKAT CELL LINE"
/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Libe Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                                                                                                                              linear EST 01-JUN-2003
LINE) Homo sapiens cDNA
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747 CGCACACCTGTACAGATGATGTACTTGCGTGAAAAGCTAAACATTGGATACATAGAAGAC
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1201 bp mRNA
ALS79236 Homo sapiens T CELLS (JURKAT CELL
clone CSODH002YJ05 3-PRIME, mRNA sequence.
ALS79236.2 GI:31317520
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Homo sapiens (human) Homo sapiens ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Butheria, Primates, Cararrhini, Hominidae, Homo. 1 (2016) 1 (2016) 1 (2016) 1 (2016) 1 (2016) 1 (2016) 1 (2016) 1 (2016) 1 (2016) 2

Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12892068.
Contact: Genoscope
Contact: Genoscope
BP 191 91006 EVAY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invircogen. This sequence belongs to sequence cluster 9202.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=cSODIO68BF01NP1&cluster=9202.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllngth.invirtogen.com/ invircogen Corporation 1600
Faraday Avenue Genoscope gequence ID: CSODIO68BF01NP1. 1. 990

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872 TGAAATTGCCGATGTCCACTGCCTTGGAGCTGCTGGAAAGTGAAATAACCTATGACAA Gaps 49.7%; Score 947.6; DB 9; Length 990; 96.7%; Pred. No. 1.2e-166; tive 18; Mismatches 14; Indels 1 Query Match Best Local Similarity 96.74 Matches 957; Conservative

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                                                  TCAGAGAATAACCAGAGAACAACCAGATTGAAACAATGGAGGATCTTTGTGTGGCAAACA
                                                                       123 CACTCTTGCCCTCAATTTATTCAAGCATCTGGCAAAAGCAAAGCCACCACCAGAACTCT
                                                                                                                                                                                        TCCTCTCCCCATGGAGCATCTCGTCCACCATGGCCATGGTCTACATGGGCTCCAGGGGCA
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                 Gape
97.9%; Pred. No. 7.3e-164;
ive 4; Mismatches 13;
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Oy 1304 ACCCTAAAACTAAGCGTGCTTCTGCAAAAGATTTTTGTAGATGAGCTGTGTGCTCA 1363	OY 1364 GAATTGCTATTTCAAATTGCCAAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCT 1423	452 GAACAACTICTGCTACCCACTAAATAAAACACAGAAATAATTAGACAATTATTTTTTTT	0   0   0   0   0   0   0   0   0   0	OY 1724 AATAAGTAGGTATCCCTCCATGCCCTTCTGTAATAATATCTGGAAAAAACATTAAACAA 1783  152 AATAAGTAGGTATCCCTCCATGCCCTTCTGTAATAATATCTGGAAAAAACATTAAACAA 93  OY 1784 TAGGCAAATATTATGTTATGCTGTTTCTAGAAATACAAAACATATATAT	RESULT 11 AL553610 AL53610 AL553610 L553610 AL553610 AL553610 AL553610 AL553610 AL553610 AL55	rce
LISTGG38/C ALSTGG38 SOCUS ALSTGG38 SPINITION ALSTGG38 Home sapiens PLACENTA COT 25-NORMALIZED Home sapiens CDNA clone CSODIO798YH02 3-PRIME, mRNA sequence.	rtebrata	Princtes; Catarrhin; Hominidae; Homo. Jessee, J. and Polayes, D. braries and normalization s sequence version replaced gi:12938977.	Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 ENRY cedex - France BP 219 91006 ENRY cedex - France BP 219 91006 ENRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr, Web: www.genoscope.cns.fr, Web: sequence Invitrogen. This sequence belongs to sequence more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODIO78DDO1NP1&cluster Feng Liang Email: fliang@lifetech.com URL: http://tullength.invitrogen.com/ InvitroGen Cor Faraday Avenue Genoscope sequence ID: CSODIO78	FEATURES  1991 /organism="Homo sapiens" /mol type="Ranka" /mol type="Ranka" /db xref="texon:9606" /dlone="CSODIO178YH02" /tissue type="PLACENIA COT 25-NORMALIZED" /clone lib="Homo sapiens PLACENIA  /cl	Ouery Match  Best Local Similarity  96.7%; Pred. No. 1.5e-163;  Batches 959; Conservative 8; Mismatches 23; Indels 2; Gaps 2;  884 TGTGCCACTGGCTGGAGCTGCTGAAATAACTAACTAACTCAACTCAACAGGG 943  991 TGTGCCACTGGCTGGAGCTGCTGAAAATAACTATGACAACTCAACAGGG 932  994 GACCAGCAAAGACAAAATGGCTGAAAATGAATAACTATGACAACTCAAAATT 1003  995 GACCAGCAAAGACAAAATGGCTGAAGATGAAATAACTATGACAAATT 1003  996 GACCAGCAAAGACAAAATGGCTGAAGATGAAATAACTATGACAAATT 1003  997 GACCAGCAAAGACAAAATGGCTGAAGATGAAATAACTATGACAATT 1003  998 GACCAGCAAAGACAAAATGGCTGAAGATGAAATAACAACTCAAATT 1003  999 GACCAGCAAAGACAAAATGGCTGAAGATGAAGAATGAAATAACAATTAAATT 1003  990 GACCAGCAAAGACAAAATGGCTGAAGAATGAAAATGAAATTAAAATTAAATTAAAATTAAAAATTAAAAATTAAAA	Db 632 TCTTTCTCTTATTATGCATAAGATAACCAACTGCATTTTATTTTTCGGCAGATTTTCTTC 573

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BX396200 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI013YO22 5-PRIME, mRNA sequence.
BX396200 BX396200 GI:30628769
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/ Organism="Homo sapiens"

/ Organism="Homo sapiens"

/ Ab zref="tax0x":

/ Clone="CS0101313V022"

/ Clone="CS0101013Y022"

/ Clone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/ Orlone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/ Orlone Tib= Thomo sapiens PLACENTA COT 25-NORMALIZED"

/ Note="Ist strand cDNA was primed with a NotI-oligo(dT)

/ Note="Ist prime end enriched, double-strand cDNA was

pliner: Five prime end cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 1041)
11, W.B., Gruber, C., Jessee, J.; and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bmail: 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9202.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
chtp://www.genoscope.cns.fr/
Feng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO13BHI1QP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.9%; Score 913; DB 13; Length 1041;
llarity 91.1%; Pred. No. 3.3e-160;
Conservative 68; Mismatches 18; Indels 1.
                                                                                            1000
                                                             900 GAGCTGCTGGAAAGTGAAATAACCTATGACAAACTCAAC
                                                                                  GAGCTGCTGGAAAGTGAAATAACCTATGACAAACTCAAC
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AUTHORS
TITLE
JOURNAL
COMMENT
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//organism="Homo sapiens"
//db xref="mexna"
//db xref="texna"
//db xref="texna"
//dlone="CSODIO78YH02"
//clone="Type="PIACENTA COT 25-NORWALIZED"
//clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
//note="Ist strand cDNa was primed with a NotI-oligo(dT)
//primer. Five prime end enriched, double-strand cDNa was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                          1; Gaps
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Best Local Similarity 99.8%; Pred. No. 1.6e-162;
Matches 937; Conservative 0; Mismatches 1; Indels 1;
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Homo sapiens (human)

Homo sapiens

ENARAYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ENARAYOLA; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1201)

S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length CDNA libraries and normalization

I (npublished (2001)

On Reb 15, 2001 this sequence version replaced gi:12900443.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Genoscope - Centre National seasonstructed by Life Technologies, was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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ALSS7133 Homo sapiens T CELLS (JUXXAT CELL LINE) Homo sapiens CDNA
Clone CSODH002YJOS 5-PRIME, mRNA sequence.
ALSS7133
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                                             TARARICCATTCATCCTCCGCTCTCTCAGCTCTGCAATCAATGCATCCACAGGGAATTA
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               361 CATGCAGCAGATCCAGAAGGGTAGTTATCCTGATGCGATTTTGCAGGCACAARCTGCAGA
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                                                                                                               TITACTGGAAAGTGTCAATAARCTGTTTGGTGAGAAGTCTGCGGGAGCTTCCGGGAAGAAWA
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//organism="Homo sapiens"
//organism="Mon"
//ob xref="taxon.9606"
//clone="CSODH002vJ05"
//clone="T.CELLS (JURKAT CELL LINE)"
//clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
//clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
//note="Voctor: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-ollgo(dT) primer. Five prime end enriched
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                             Contact
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9202.f For more information about this cluster, see http://www.genoscope.cna.fr/
cgi-bin/cluster.cgi-Secq-CSOBHO02CE03OP1&cluster=9202.f. Contac Feng Liang Email : fliang@lifetech.com URL : http://full.ength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOBHO02CE03OP1.
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1 (bases 1 to 989)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                   402 TCCATTCATCCTTCCGCTCTCTCAGCTCTGCAATCAATGCATCCACCACAGGAATTATTTAC
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                                                                                                                                                                   TCCATTCATCCTTCCGCTCTCTCAGCTCTGCAATGATGCATCCACAGGGAATTATTTAC
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130 GCCCCACCCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGCCATGGTCT
162 GCCCCACCCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGCCATGGTCT
                                                                         ACATGGGCTCCAGGGCAGCACCGAAGACCAGATGGCCAAGGTGCTTCAGTTTAATGAAG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I cuber, C., Jessee, J. and Polayes, D.

15 Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

16 Pull-langth cDNA libraries and normalization

17 Inpublished (2001)

18 Contact: Genoscope

18 Contact: Genoscope

19 19 1006 EVRY cedex - France

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10 Invitrogen. This sequence by Life Technologies, a division of Invitrogen. This sequence blongs to sequence cluster 9202.f For more information about this cluster, see http://www.genoscope.ons.fr/

10 cgi-bin/cluster.cgi?seq=CSD1021DE09QPl&cluster=9202.f. Contact : Feng Liang Email : fliangelifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0D1021DE09QPl.
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/db treef="taxon:9606"
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primer. Five prime end enritched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized.
                   CCTTTCCGTGTAAACTCGGCTCAGCGCACACCTGTACAGATGAGATGTACTTGCGTGAAAAG
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 REFERENCE AUTHORS		ng, P.E	:		arter, K.C.,	Ebner, R., Endress, G.,
TITLE		Horrigan, S. Cancer gene	. e	ming	, Soppet, D.R. and Weaver, Z. determination and therapeutic	c screening using signature

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Avalon Pharmaceuticals (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                             Score 3116.4;
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2617 CCCCACTGCAGCAGCACACCAATAAGAAACTGCTGCTTCAAGGTAGCTGCTTCTAAGGTAGCTTCTAAAAAACTGCACTGCTTCAACTGCGGGTTTCTAG 2401 CCCCACTGCAGCAGCACACCAATAAGAAACTGCTGCTTCAAGTGCTGCTCCCAAAC 2461 CCCCACTGCAGCAGCACACCAATAAGAAACTGCTGCTCTGCTCCCAAAC 2462 CCCCACTGATTGATTGATTGATTAACTAATAACCCCAATGCAAACTGCTCTGCTCCCAAAC 2521 TTCTGACTTGACTGAACTGCACTAACTTTTCAATATCCAGGAAACACTCTGCTCCCAAACC 2521 TTCTGACTTGACTGCACACAGAACCCTTTCAGAACAACTCTCTGGAAAACCAATTTTTTTT	RESULT 4 HUMCDSM LOCUS DEFINITION Human aorta caldesmon mRNA, complete cds. ACCESSION WB3216.1 Galdesmon. RB3216.1 Galdesmon. RB3216.1 Galdesmon. RB3216.1 Galdesmon. RB3216.1 Galdesmon. RB3216.1 Galdesmon. SOURCE From sapiens Frayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai, Butheria; Primates; Catarrhini; Hominidae, Homo. REFERENCE Humphrey, M.B., Herrera-Sosa, H., Gonzalez, G., Lee, R. and Bryan, J. TTLE Cloning of cDNAs encoding human caldesmons JOURNAL Gene 112 (2), 197-204 (1992) REDINE PUBNED 1555/69 COMMENT On Jul 26, 1993 this sequence version replaced gi:180193. Original source text: Homo sapiens adult aorta cDNA to mRNA. FEATURES Location/Qualifiers
1537   AAGGCCACACACACACACACACCACACCACACACACACA	2317 AGATGGCTTGTCAGATGACATCATCAAGTGTTTCACTCCTAAAGGTTCATCT 2376 2101 AGATGGCTTGTCAGATGACAAGAAACCATTCAAGTTTCACTCCTCAAAGGTTCATCTCT 2160 2377 CAAGATAGAAGAGCAGAATTTTTGAATAAGTGTTTCACTCCTCAAAAGCTTCATCT 2160 2161 CAAGATAGAAGAGCAGAATTTTTGAATAAGACTGGACAAAAGCAGTGTTCAA 2220 2437 ATCGACCCATCAAGCAGAATTTTTGAATAGATTGACAGAAAAGCAGAAAAGCAGTGTACCAG 2496 2437 ATCGACCCATCAAGCAGCAATAGTTCCCAAGATTGACAGACA

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2281 TGCAATTGAGGGAACAAAAGGGGA 2557 TCCTGCTGAAGGTGTACGCAACATC 2617 CCCCACTGCAGGGGACACACACACACACACACACACACAC	RESULT 5 G28707 G28707 DEFINITION 8WS3978 Eric D. Green Homeon site. ACCESSION G28707 REYWORDS STS. SOURCE Homeon sapiens (human) ORGANISM Homeon sapiens (human) MAMMALIA: Eutheria; Primate Mammalia: Eutheria; Primate Nathors AUTHORS Bouffard, G.G., Iyer, L.M., I
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2	2857	ACGCAGGACGAGCTCAGTTGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTGATTT 2916
Db 2	2641	ACGCAGGACGAGCTCAGTTGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTTGATTT 2700
7 7 20 20 20 20 20 20 20 20 20 20 20 20 20	2917	ACTAAATTGGGTTCATTATTTTTTTCAATATCCCAGTAAACCCATGTATATTG 2976 
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Oy Db	3037	AGCCTGTTTCTAAAGAAACCCATGCTGTGAAATAGAGACTTTTCTACTGATGATGATAAC 3096
φ <sub>γ</sub>	3097	TCTGTATCTGAGCAGTGATACCACACCACATCTGAAGTCAACAGAAGATCCAAGTTTAAAA 3156
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3	3157	21
Dp 2	1941	iig-cigcogaaigigcagiaiciagaaaaaagaaccgiagiiitigiiititaaai 2999
	3217	ACAGAAGTCATGTTTCTGCACTTTATAATAAAGCATGGAAGAATTATCTTAGTAGG 3276
e aa	2	0 1
33	277	m
Dp 3	0901	caaitigtaacacttritigaaagtaacccatticagattigaaatactgcaataatggttg 3119
3	1337	CITIAAAAAAAAAAAAAAAAAAGAIGCGGGGAGAGIIAITCCTII 3378
Db 3	1120	tcittaaaaaaaaaaaaagaatgiacigitaaggiaitacitit 3161
RESULT 5 G28707 LOCUS DEFINITION	රිකිරි	28707 3610 bp DNA linear STS 28-SEP-1998 8533978 Eric D. Green Homo sapiens STS genomic, sequence tagged
ACCESSION VERSION KEYWORDS		G28707.1 GI:1408143 STS
ORGANISM	ដែយ៍ទ័	omo espiens (meman) omo espiens ikaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; mmalia: Butheria: Primates; Catarrhini; Hominidae; Homo.
REFERENCE AUTHORS		.M., Idol,J.R., Braden,V.V., Cun

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Information about the WHGRI chromosome 7 mapping project, see http://www.nhgri.nih.gov/DIR/GTB/CHR7. Also see Genomics 11:548-64 (1991) [MUID=92128937].

Location/Qualifiers 1. .3610 /organism="Homo sapiens" /molltype="genomic DNA" /molltype="genomic DNA" /db xref="taxon:9606" /molltype="genomic DNA" /molltype="gen
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Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.
Leckte,M.P. and Green,B.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
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	1321		ACATACTGAGAATACTTTCAGCCGCCCTGGAGGGGCCAGCGTGGACACCAAGGAGGGCCAGCGTGGACACCAAGGAGGGCCAGCGTGGACACCAAGGAGGGCCAGCGTGGACACCAAGGAGGGCCAGCGTGGACACCAAGGAGGCCGCCTGGAGGGCCAGCGTGGACACCAAGGAGGCCGCCCCCCAGGTGGAAAGGCTGGAGGGCAGGGGGGGG	CCTGGAGGAACTCAAGAAAAGAGGGAGGAGAAAGGAAGGTCCTGGAGGAAGGA	2317 AGATGGCTTGTCAGATGACAATACCATTCAGTGTTTCACTCCTAAAGGTTCATCTCT 2376 2101 AGATGGCTTGTCAGATGACAAGAAACCATTCAAGTGTTTCACTCCTAAAGGTTCATCTCT 2160 2377 CAAGATAGAAGAGAGAATTTTTGAATAGTCTGTGCAGAAAAGGTGTTCATCTT 2160 2377 CAAGATAGAAGAGCAAGATTTTTTGAATAAGTCTGTGCAGAAAAGCAGTGTCAA 2436 2161 CAAGATAGAAGAGCAGAATTTTTTAAATAAGTCTGTGCAGAAAAGCAGTGTCAA 2220 2437 ATCGACCCATCAAGCAGAATAGTCTCAAAAAGCAGAAAAGCAGTATACCAA 2496

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### Warmwalla, Entheria; Printes, Catarthili, Moninidae, Homo.  ### Warmwalla, Entheria; Printes, Catarthili, Moninidae, Homo.  ### TYTES  ###		CGAAGGATGAAAAAAAGACAAAGAACCCAAAGAAGAGTTAAGAGCTTCATGGA CGAAAGAAGAAGAATTAACAGAAGAAGTCCCAAAGAAGAAGATTAAAGAGCTTCATGGACTTCAAAGAAGATTAAAAAAGAAGTTAAGTCGCAGAAATGATGAAGAATTCATGACCCACAAATTCGAAAGATTAACAAAATTACAAGAATTAAAGAATTCATGACCACCAAAAATTAAAAAAAA	GGGGAGGCCCCCCCGGGGGGGGGGGGGGGGGGGGGGGG	2254 GCTAAAGGAGAGCGAAGGCGAGAGCTCTGAAAGCCCAGAAGATCC 2313 1208 GCTAAAGGAAGATTGAAAGCCAAGAGCTGCTGAAAGCCCCAGAAGATCC 2313 1208 GCTAAAGGAAGAGATTGAAAGCCAAGAGCTGCTGAGAAGATCCC 1267 2314 AGAAGATGGCTTGTCAGATGACAAGACCATCAAGTTTCACTCCTAAAGGTTCATC 2373 1268 AGAAGATGGCTTGTCAGATGACAAACCATTCAAGTGTTTCACTCCTAAAGGTTCATC 2373 1329 TCTCAAGATGAAGAGCAAAACCATTTTGAATAAGTCTGTGCAGAAAAGTGGTT 1384 2434 CAAATCGACACAACAAAAGCGAATTTTTGAATAAGTCTGTGCAGAAAAGTGGTT 1384 2434 CAAATCGACCCATCAAGCAATAGTCTCCAAGATTGACGAGACTGCAGAATAC 2493 1385 CAAATCGACCCATCAAGACAATAGTCTCCAAGATTGACGAGACTGCAGAACTATAC 1444 2494 CAGTGCAATTGAGGGAACAAAAGCGCAAAACCTACAAAGCCGCAGCCTCGAGCTATAC 1444 2494 CAGTGCAATTGAGGGAACAAAAAGCGCAAAACCTACAAAGCCGCAGCCTCGGATTAC 1504 1445 CAGTGCAATTGAGGGAACAAAAAGCGCAAAACCTACAAAGCCGCCAGCCTCGGATTTCC 2553 1416
Numeralist Butheris; Primates; Ctarrhini, Hominides; Homo.  1	8 8 8 8 8 8 8 8 8	: 6 6 6 6 6 6	8 6 8 6 8 6 8	6 8 6 8 6 8 6 8 6 8 6 8 6
Nammalia, Entheria; Primates; Catarnhini, Hominidae; Homo.  (bases 1 to 403)  Lobase 1 to 403)  The Carman Annah Comportion  The Carman Annah Comportion  Neither Carman Annah Comportion  Neither Carman Card Card Card Card Card Card Card Card				
ଞ୍ଚି ହିଲ୍ମି <b>ର</b> ୁ ଜୁଣ ହୁଣ ହୁଣ ନ୍ତି ନ୍ତି ନ୍ତି ନ୍ତି ନ୍ତି ନ୍ତି ନ୍ତି ନ୍ତି	Mammalia, Eutheria; Primates, Catarrhini; Hominidae; Homo.  1 (bases 1 to 4091)  S Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,  Robo, G., Han, M. and Wiemann, S.  The German Human cDNA Consortium  Direct Submission  Submitted (27-Aug-2003) MIPS, Ingolstaedter Landstr.1, D-83764  Neuherberg, GERMANY  Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de;  sequenced by Qiagen (Hilden/Germann) within the cDNA sequencing  consortium of the German Genome Project.  This clone (DKEZD668A06190) is available at the RZPD in Berlin.  Please contact the RZPD: Reseaucentrum, Heubnerweg 6, 14059  Berlin-Charlottenburg, GERNANY; Email: clone@rzpG.de Further  information about the clone and the sequencing project is available  at http://misps.gsf.de/proj/CDNA/.	/mol_type="mRNA" /db_xref="reaxon:9606" /map="7g3" /clone="DKFZp686A06190" /tlease type="human escphagus tumor" /clone_Lib==686 (synonym: hlcc3). Vector pSport1_Sfi; DH10B; Bites SfilA + SfilB" /dev_stage="adult" 4069 4069 60.0%; Score 2222.6; DB 9; Length 4091;	rily  S6.5%; Pred. NO. 0;  nservative  0; Mismatches  19; Indels  56; Gaps  Adgardacaadgadadadadadadaccaaagccaaagccar  Addadacaadgadadadadadadadadadadadadadadad	GAGGGAACAAGGTTCAGATTTCCCATCATGAAAAGATGGAAGAGGAAGACAAGGA           GAGGGAACAAGGTTCAGATTTCCCATCATGAAAAAATGGAAGAGAAGACAAGGA           AAGAGGAACAAAGGTTCAGAAGCAAAAAAAGAAGAAAATTAAAGCCGA           AAGAGCTGAGGCAAGGTTTCCCATCATGAAGAAAAAAAGAAATTAAAGCCGA           AAGAGCTGAGGCAAGGTTTCAAAGAAGAAAAAAAAAAAA

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Hayashi.K., Hashida.T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
DNA encoding a protein comprising calmodulin-and actin-binding
human caldesmon peptide fragment
Patent: US 573008-A H 14 A-APR-1998;
Location/Qualifiers
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                                                    TAGCCGCATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAA
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Score 1570.2;

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Query Match

ORIGIN

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS TITLE

JOURNAL FEATURES

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1901 AAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACAT 1960
                              KATOU IKUNOSHIN, SOFUE KENJI
CO7KI3/00,C12N15/12//A61K37/02,C12P21/02,G01N33/53,(C12P21/02,
C12R1:19);
strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 CAAGAAAGATAGGAGATAGAGGAAACAGAAACAGTCACCAAGTCCTACCAGAAGAATGAT
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                                                                                                                                         topology: Linear;
*source: cell_type=Hela;
Key Location/Qualifiers
                                                                                                                                                                                                                                                   CDS 12. .1688

/product='human ca
polyA_signal 2103. .2108
polyA_site 2199. .2215.
Location/Qualifiers
1. .2215
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xxef="taxon:9606"
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42.4%; Score 1570.2;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches
2141
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                                                                                           TATITAATAATCACAGTCTAGAGATGTTCATGGTAAAAGTACTGCCTTTGCACAGGAGCC
                                                            ATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCT
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SCFUE KENJI, TAKARA SHUZO CO LTD
OS Homo sapiens (human)
PN JP 1992230099-A/3
PD 07-SEP-1993
PF 27-DEC-1991 JP 191158040
PR 29-MAR-1991 JP 91P 89106
PR 49-MAR-1991 JP 91P 89106
PR 49-MAR-1991 JP 91P 89106
PR 49-MAR-1991 JP 91P 89106
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Hayashi,K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
Proteins comprising calmodulin- and actin-binding human caldesmon
polypeptide fragments
Patent: US 553237-A 14 02-JUL-1996;
Location/Qualifiers 1781 GCTAAAAGAGAAAAGCTCCAAGAAGACGAAGCCTACCTTCAAAAAGAAGAAGATCAAAAGAT GAAAAAGATTAAAAAGGACAAAAGAACCCAAAGAAGAAGTTAAAGAGCTTCATGGATCGAAAG 702 GAAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG 762 AAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACAT 1961 ACTGAGAATACTTTCAGCCGCCCTGGAGGGAGGGCCCAGCGTGGACACCAAGGAGGCTGAG 882 ecceccococacarcada a cocacada a cocacada a cocacaca a cocaca a cocaca a cocacaca a cocacaca a cocacaca a cocacaca a cocaca a cocacaca a cocaca a cocaca a cocaca a cocaca a cocacaca a cocaca a cocaca a cocaca a cocaca GAGGAACTCAAGAAAAAGAGGAGAGAGAAGGAAGGAAGGTCCTGGAGGAAGAAAAGAGCAGAGG ACTGAGAATACTTTCAGCCGCCCTGGAGGGAGGGCCAGCGTGGACACCAAGGAGGCTGAG GGCGCCCCCCAGGTGGAAGCCCAAAAAGCCTGGAGGAGCTTCGTCGTCGTCGTCGCGGGAG 2201 AGGAAGCAGGAGGAAGCCGATCGAAAACTCAGAGAAGAAGAAGAAGAAGAAGAAGAAG CAAGAAAGATACGAGATAGAGGAAACAGAAGTCCACCAAGTCCTACCAGAAGAATGAT GATAAACTTCAGACAGCTGTCCTAAAGAAACAGGGAAGAAGAAGGAAACTAAAAGTGCAA 4; Gaps PAT Length 2215; 93; Indels linear 9 DB DNA Query Match 42.4%; Score 1570.2; Best Local Similarity 94.5%; Pred. No. 0; Matches 1660; Conservative 0; Mismatches 2215 bp 1 US 5532337. 2215
 organism="unknown"
 mol\_type="unassigned DNA" 123421 Sequence 14 from patent 123421 I23421.1 GI:1603291 Unknown. Unclassified. Unknown 2321 ò

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (basea 1 to 4130)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Mallahy, S.J., Boask, S.A., McEwant, F.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wanzh, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Schait, J. Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse oDNA sequences

Nather Stand Sci. U.S.A. 99 (26), 16899-16903 (2002)
         4130 bp mRNA linear PRI 07-0CT-2003
Homo sapiens caldesmon 1, transcript variant 3, mRNA (cDNA clone
MGC:21352 IMAGE:4753285), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15149468.
Location/Qualifiers
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/mol type="mkNA"
/mol type="mkNA"
/clone="MGC:21352 IMAGE:4753285"
/tissue type="%kin, squamous cell carcinoma"
/loone lib="NCI CGAP_Skn4"
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1182 GGCTTGTCAGATGACAAGAAACCATTCAAGTGTTTCACTCCTAAAAGGTTCATCTCTAAG
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DLRPGDVSSKRNLWEKQSVDKYTSPTKY" 2115 2175 ACAGAAGTCATGTTTTCTGCACTTTA 3244 AACCTGTTTCTAAAGAAACCCATGCTGT 3064 3124 3184 SCAATTGTAACACTTTTGAAAGTAACCC 3304 PRI 18-DEC-2002 rakeuchi, R., Takeda, O., Asada, K., niata; Vertebrata; Euteleostomi; arrhini; Hominidae; Homo. ue, Osaka University, Medical rr, Department of Neurochemistry seka 530, Japan 5-6879) SCTTTAAAAAAAAGAAAA 3354 ldesmon gene (24), 12122-12126 (1992) mRNA linear I, complete cds.

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B 3; AA 1660 AT 521 AA 1720 AA 1780 AA 641	AT 1840 AT 701 AG 1900 AG 761 AG 761 AH 1960 AT 821		TG 1001 GG 2200 GG 1061 AG 2260 AG 1121	AT 2320 	CC 2620 CC 2620 CC 2620 CC 2620 CC 2620 CC 2680
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/tisque_type="lung"

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Best Local Similarity 96.6%; Pred. No. 0;
Matches 1555; Conservative 0; Mismatches 55; Indels
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                    1 (bases 1 to 2137)
Hayashi,K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
Hayashi,K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
DNA encoding a protein comprising calmodulin-and actin-binding
human caldesmon peptide fragment
human caldesmon peptide fragment
Patent: US 5739008-A 13 14-APR-1998;
Location/Qualifiers
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Score 1481.6; DB 6; Length 2137;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hayashi, K. and Sobue, K.
Hayashi, K. and Sobue, K.
Direct Submission
Submistred (5-JUL-1991) Kenji Sobue, Osaka University, Medical
School, Biomedical Research Center, Department of Neurochemistry
and Neuropharmacology; Kita-ku, Osaka 530, Japan
(Tel:81-6445-6879, Fax:81-6-6445-6879)
Location/Qualifiers
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Best Local Similarity 96.5%;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
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ABQ55690
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The present invention describes a method (MI) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AbleGe64 to Abl70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cyrostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocationem, carcinoma, class cells cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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Best Local Similarity 99.3%; Pred. No. 0;
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                                          28-SEP-2000; 2000US-0236111P.
29-SEP-2000; 2000US-0236842P.
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Weaver Z;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
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                                                                      CCGCATCAATGAATGCTAACTAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACC
                                                                                                                     CTGACTTGAGACCAGGAGGCGTATCCAGCAAGCGGAAACCTCTGGGAAAAGCAATCTGT
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                                          CCGCATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACC
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ABL68604
ID ABL68604 standard; DNA; 3610 BP
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AC ABL68604;
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DT 15-MAY-2002 (first entry)
XX
DT Homey cancer related gene sequency
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WH Human; cancer; colon; breast; ok whomach; lung; prostate; pancre
XW stonach; lung; prostate; pancre
XW gene; ds.
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NO200194629-A2.
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ND 13-DEC-2001.
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                                                                       01-NOV-2000; 2000US-0245084P
                                7-SEP-2000
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US-0237278P

## (AVAL-) AVALON PHARM.

Horrigan S; Ebner R, Endress G, Carter KC, Augustus M, Weaver Z; Young PE, Soppet DR,

## WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

## Claim 1; SEQ ID NO 6941; 44pp; English

The present invention describes a method (M1) for screening for an anticomplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
comprises in indicative of anti-neoplastic activity. (I) has cytostatic
comprises in a to least 195% identical to (S), where a change in
comprises on the act least 95% identical to (S), where a change in
comprises of the act of anti-neoplastic activity. (I) has cytostatic
anti-neoplastic agent, and can be used for producing a product which is
contivity and can be used in anti-neoplastic agent as a result
of M1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney,
prostate or pancreatic cancer, adenocarchoma, clear cell
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

SXS	C tumour X C commence 3610 RD: 1322 A: 622 C: 963 G: 703 T: 0 U: 0 Other:	
, 8ª	Query Match 84.2%; Score 3116.4; DB 6; Length 36 Best Local Similarity 99.3%; Pred. No. 0;	
ğ.	Matches 1140; Conservative 0; Mismatches	CAPE TOTTO 27
g 6	1 CCIGCCIGCCCGCCTGCTTCTCTCTGGCTGTGCTCTGCTTAAAGAAAT	. 0
È	y 277 TITCGGACTTAGTCCTCGGGAAGAAGTTTCAGACTACAAGGTATCATTGGAAC	ATTTCAA 33
ор	61 TTTCCGACTTAGTCCTCGGGAAGAAGTTTCAGACTACAAGGTATCAT	ATTTCAA 12
· 장 점	y 337 GATCATCAAATTCCACAGGGATTGGTGACCAACCAGAAGGCTCAGACTCAGACTCAGACTCAGACTCAGACTTCCACAGGGATTGGTGACCAACCA	ATCTGATT 396           ATCTGATT 180
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8	457 T	GCAGAAAG 516
Q	241 T	GCAGAAAG 300
ò	N 517 AATGGCTACCAGAGAATGACGATGATGAAGAAGGAGGCAGGC	56 57
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ò	57	GTGACCGA 636
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දි දි	2y 637 CCAGGTGGAGGTGAATGCCCAGAACAGTGTGCCTGACGAGGGGCCAAGACAACACCACACACA	ACCACCAC 696           ACCACCAC 480
ઠે	27 697 AAACACTCAAGTGGAAGGATGATGAGGCGCACATTCCTGGAGGCCTGGGTCGGCGTGA	75
đ	481	5 4
à	75	GACCCAAC 816
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දු පු	2y 817 AATAACAGATGCAAGTCTCGCTCCCAACAGAATGCAAAATGAAATGAAAATGAAAAAAAA	99
ò	OY 877 TGAAACTACCGAGAAGAAGAAAAAGTGAAAGAGTCGCCAAGAAAGA	93
g	661 TGAAA	72
ò	QY 937 AACAGAAACAGTCACCAAGTCCTACCAGAAGAATGATTGGAGGGATGCTGAAGAAAACAA	99
d d	721	780
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දු පු	OY 1057 AGAAATCAGGTAGAGGTGATGATGAGAAAACAACTGAAAACCAGAAAGAA	GGAACAGT 1116             GAAACAGT 900
ò	1117	3GAGGAGAG 1176
g	901 GGTAATGTCATTAAAAATGGGCAGATCAGTTCAGAAGAGG	SCAGGAGAG 960
δ	Qy 1177 GGAACAAGGTTCAGATGAGATTTCCCATCATGAAAAGATGGAAGAGAAGAAGAAGAAAG	DAAGGAAAG 1236

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                       Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 3140; Conservative 0; Mismatches 21;
                                                                                                                                                              Gene #2407 used to diagnose liver cancer
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                                                                    ABN95909 standard; DNA; 3610
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3156 2940 3216 2999 3276 3059 2580 2640 2700 2976 2760 3036 2820 3096 2880 2856 2520 2796 ACTADATTGGGTTCATTATCTTTTTTTTATATCCCGGTADACCCATGTATATTATC TIGCCIGCGGAAIGIGCAGIAICIAGAAAAIGAACCGIAGIIITIGIITITIAAAI ACAGAAGICAIGITGITICIGCACITIAIAAIAAAGCAIGGAAGAAITAICITAGIAGG 2701 ACTABATIGGGTTCATTATCTTTTATTTTCAATATCCCAGTAAACCCATGTATATTTTC TCTGTATCTGAGCAGTGATACCAACCACATCTGAAGTCAACAGAAGATCCAAGTTTAAAA TTG-CTGCGGAATGTGTGCCAGTATCTAGAAAATGAACCGTAGTTTTTGTTTTTTAAAT CAATTGTAACACTTTTTGAAAGTAACCCATTTCAGATTTGAAATACTGCGATAATGGTTG 2857 ACGCAGGACGAGGTTGTAGAGGCCTAATICGCTCTGTTTTGTATTTATGTTGATTT CCCCACTGCAGCAGCACACCAAATAAGGAAACTGCTGGCTTGAAGGTAGGGTTTCTAG TTCTGACTTGAGACCAGGAGACGTATCCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGT 3337 CTTTAAAAAAAAAAAAAAAGATGCGCCGACAGTTATTCCTTT 3378 3120 rcirraaaaaaaaaaaaaaaacaarraaagararracirir

BESULY 4
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D Differentially expressed breast cancer associated cDNA
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04-OCT-2001; 2001US-00974298
                        WPI; 2003-182653/18.
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                  Chen H;
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New cDNAs, which are differentially expressed in (metastatic) breast cancer useful for diagnosing or staging, breast cancer, or for monitoring the treatment of breast cancer in an individual.

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Claim 1; SEQ ID NO 36; 30pp; English

The invention describes a combination of CDNAs (designated BC-CDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-CDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or burifying antibodies from a sample. The antibodies, which specifically bind the protein differentially expressed in breast cancer is useful for descring the expression of a protein in a sample. The BC-CDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast cancer associated CDNA. Note: The sequence data for this patent did not format directly from the US patent office at

segdata.uspto.gov/sequence.html?DocID=20020156263

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Sequence 4547 BP; 1496 A; 849 C; 1033 G; 1169 T; 0 U; 0 Other;

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563 539 119 179 239 323 299 383 359 443 419 503 479 203 263 AAGTTTCAGACTACAAGGTATCATTGGAACATTTCAAGATCAAATTCCACAG TCATTGGCTGCCTATTAGAAAACGACAAGACAATGCATACCACCGCCTCCCGACTGTAA acaragoggararcificacriagcarggacricifoggagoggoccaaggaaggoggic aagititcagactacaaggtatcattggaacatttcaagatcatcaaaattcaacag GGTCTCCCTGAACCTGAAATCACACATGGATGATTTTGAGCGTCGCAGAGAACTTAGAA TCATTGGCTGCCTATTAGAAAAACGACAGGACAATGCATACCACGGCTCCCGACTGTAA reregerrerectrocrectranaganarcagrectrecerreceaerregeang rcheecrerectectraaasaaatcactroctroccactractecasas GGATTGGTGACCAACCAGAAGGCTCAGACATCTGATTGCTGACCTGTCCAGACATCATCT GCCTAGGGAATGACAGGCATCTCCACAGGCAGGCTGCATCCACCTT-GGCTGGGGGTGTCG Gaps Length 4547; 166; 9; Indels DB 7; Score 1793.6; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 76.9%;
Matches 2585; Conservative 444 420 504 264 240 300 384 360 480 84 9 144 120 204 180 324

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1499 1148 1148 1559 1019 1103 1080 TGGAAGAGAAAACAACTGAAAGCCAGGAGAAACAGTGGTAATGTCATTAAAAAATGGGC 1139 1199 1260 TGGAAGCAGAAGAAAGAAAGAATTAAAGCCGAGCAAGACAAAAAAAGATAGCAGGATGAAC 1319 1043 839 899 959 779 863 923 983 683 629 743 719 803 CAGCAGAGGAGGAGGATAAAAGAGGAAGAAAAAGGGCAGCAGAGGAGGAGGAGAAAA 1440 AGGAGGAAGAAAAAGGCCAGCAGCAGGAGGCAGAGGATAAAGGAGGAAGAAAAAGG 1560 GGGCCAGGGCAGAGGAAGAAGAAGACTAAGGTAGAAGAGCAGAAACGTAACAAGCAGA AGATCAGTTCAGAAGAGCCTAAACAAGAGGAGGAGGAGGAACAAGGTTCAGATGAGATTT 1020 AGGAGGAAGAGGAAGAAGCCAAAGGGAGGAGTTGGAGAAAATCAGGTAGAGGTGATGG 1200 CCCATCATGAAAAGATGGAAGAAGACAAGGAAAGAGAGGGTGAGGCAGAGAGGGCAAGGT Ardadecedearrecredadedecredecredecerdadadadedecenaaaacerere AGGAGGCTCTGGAGGGGGAGAGAGGAGTTCGACCCAACAATAACAGATGCAAGTCTGTCGC 900 AAAGTGAAAAGTCGCCAAGAAAGATACGAGATAGAGGAAACAGAAACAGTCACCAAGTCCT 564 GCCAAAAGAGGAGGAGAATGCGACTCGAAGCAGAAAGAATCGCCTACCAGAGAATGACG AGAAGCAGGAAGAATCCTTGGGACAGGGGACCGACCAGGTGGAGGTGAATGCCCAGA ACAGTGTGCCTGACGAGGAGGCCAAGACAACCACACAAACACTCAAGTGGAAGGGGATG ATGAGGCCGCATTCCTGGAGCGCCTCGGCGTGAGGAAAGACGCCAAAAACGTTC ATGATGAAGAGGAGGCAGCCCGGGAACGGCGCCGCCGAGGACAGGAACGGCC 924 984 096 1104 1149 1140 1149 1149 1149 1149 1149 1149 840 009 684 744 720 780 540 624 99 804

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	RESULT 5 AAQ28988 standard; CDNA to mRNA; 2215 BP. XX AC AAQ28988 standard; CDNA to mRNA; 2215 BP. XX DT 25-WAR-2003 (revised) DT 25-FBB-1993 (first entry) DT 25-FBB-1993 (first entry) DE Sequence encoding a polypeptide of human caldesmon designated type II DE (light) AA. XX Caldesmon; calmodulin; actin; binding; actomysin system; regulation; ss. XX CALDER COS (Arag= a cost) XX CALDER COS (Arag= a cost) XX CALDER COS (Arag= a cost) XX CALDER COS (Arag= a cost) XX CALDER COS (Arag= a cost) XX CALDE COS (Arag= a cost) XX CALD COS (Arag= a cost) XX DO (Arag= b cost) XX XX XX XX XX XX XX XX XX XX XX XX XX
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(SOBU/) SOBUE K. (TAKI ) TAKARA SHUZO CO LTD. 29-MAR-1991; 27-DEC-1991; Hayashi 

WPI; 1992-325651/40

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Kotani H,

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91JF-00089106 91JF-00358040 92EP-00302591

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Polypeptide(s) with calmodulin- and actin binding activities - useful for tracting and diagnosing cancer and regulating digestive tract motility as vasodilators.

Disclosure; Page 33-34; 47pp; English

a cDNA clones that encode polypeptide of human caldesmon were selected from a caid sequence encoding human caldesmon were deduced by DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis.

Cacid sequence encoding human caldesmon were deduced by DNA sequence analysis.

Call Next, the inventors prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide.

Call calmodulin-binding activity and extin- binding activity as indices. There are two forms of caldesmon. The form of higher mol. wt. is called type I and the form of lower mol. wt. is called type II. 312AA is and 118A are polypeptide that have a sequence of 116 ABs in the C-terminal sequence of 312AA, and 94AA and 90AA are polypeptides that have a sequence of 118AA there are residues Met-Ala that originated from a PCR primer, continued of 100AA, there are residues Met-Ala that originated from a PCR primer, corriginated from a PCR primer. The polypeptide of 116 AAB has both calmodulin-binding activity and actin-binding activity. Type I, type II, 312AA, 118AA, 118A

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Sequence 2215 BP; 778 A; 436 C; 593 G; 407 T; 0 U; 1 Other;

1960 GATAAACTTCAGACAGCTGTCCTAAAGAAACAGGGAGAAGAGAGAAGAAGAAGTAAAGTGCAA 1780 1900 1601 CAGAAACGTAACAAGCAGCTAGAAGAGAAAAAAAATGCCATGCAAGAGAGACAAAGATAAAA 1660 641 701 761 821 462 chagahadarhddadarhadadahadadahadadrohddadrocrhochadahadar 521 GAAAAGATTAAAAAAGACCAAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG GAAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG AAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAAACAT 762.BAGGGATITACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACAT 4 Query Match
42.3%; Score 1567; DB 2; Length 2215;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1658; Conservative 0; Mismatches 95; Indels 4 1721 1781 1841 702 1901 642

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DB 4; Length 3342, T; 0 U; 0 Other;

Sequence 3342 BP; 1108 A; 590 C; 687 G; 957

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Sequences AAH33071-23152 represent nucleic acid sequences derived from osteoarthrits tissues. The sequences are useful as probes and for the diagnosis or prognosis of mammalian osteoarthritis. The polymucleotides and holypeptides of the invention are useful for generating diagnostic reagents, as targets for small molecule drug development, generation of therapeutics, and cloning genes Specific antibodies are used to generate invented memosorbent assays for detection of osteoarthritis. The invented molecules can be used to treat osteoarthritis or to analyse the disease-modifying activity of osteoarthritis drugs. Other disorders treatable using the nucleic acid sequences include atopic, inflammatory and infectious disorders e.g. Crohn's disease and sepsis, and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substantially purified protein, polypeptide or their fragments, used to identify a biologically active compound or composition and treat mammalian osteoarthritis.
Osteoarthritis tissue-derived nucleic acid sequence #32
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                                                               3221 AAGTCATGTTTTTTTTTATAATAAAGCATGGAAGAAATTATCTTAGTAGGCAAT
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                                                                                     1931 GGAGAATTCATGACCCACAAACTTAAACATACTGAGAATACTTTCAGCCGCCCTGGAGGG
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                                         1871 GAAGAAGTTAAGAGCTTCATGGATCGAAAGAAAGGGATTTACAGAAGTTAAGTCGCAGAAT
                                                      1 GAAGAAGTTAAGAGCTTCATGGATCGAAAGAAGGGATTTACAGAAGTTAAGTCGCAGAAT
                                                                                                                                AGGGCCAGCTGGACACCAAGGAGGCTGAGGCGCCCCCCAGGTGGAAGCCGGCCAAAAGG
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Query Match
39.3%; Score 1455.8;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1482; Conservative 0; Mismatches
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                                                                                                    ATGAACCGTAGTTTTTTTTTAAATACAGAAGTCATGTTGTTTCTGCACTTTATAAT
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         CATGGTAAAAGTACTGCCTTTGCACAGGAGCCTGTTTCTAAAGAAACCCATGCTGTAAA
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                                ATATICCCAGTAAACCCATGTATATTATCACTATATTAATAATCACAGTCTAGAGATGTT
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controlled that encode polypeptide of human caldesmon were selected from a containing the cells, and the DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis. Next, the inventors prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptides. Very cand looked for the functional domain of human caldesmon polypeptides. Or using calmodulin-binding activity and actin-binding activity as indices. There are two forms of caldesmon. Wr. is called type II. 312AA is a since type I and the form of lower mol. Wr. is called type II. 312AA is and conjypeptide that is the C-terminal portion of types I and II. 122AA and colypeptide that thave a sequence of 116 As in the C-terminal colypeptides that have a sequence of 118AA that are in the central portion. On the N-terminal colypeptides that are in the central portion. On the N-terminal colypeptide for the N-terminal portion and the C-terminal portion on the N-terminal of 90AA, there are residues Met-Ala that originated from a PCR primer. Or ilsaAA, there are residues Met-Ala that originated from a PCR primer. Or the N-terminal of 122AA and 94AA, there are residues met-Ala that originated from PCR primer. The polypeptide of 116 AAS has both calmodulin-binding activity and actin-type II, type II, 1312AA, 118AA, 118AA, 118AA, 118AA, 118AA, 118AA all have tropolypeptide of 116 AAS has both calmodulin-binding activity and activity or crimonyosin-binding activity and have an inhibitory activity and activity or actomyosin ATPase, and so the functional unit of human caldesmon is identified as being 116AA. (Updated on 25-MAR-2003 to correct PN field.)
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      Polypeptide(s) with calmodulin- and actin binding activities - useful for treating and diagnosing cancer and regulating digestive tract motility as vasodilators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     835 TGGAGGAGCTTCGTCGTCGTCGCGGGAGACCGAGAGCGAAGAGTTCGAGAAGCTCAAAC
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Best Local Similarity 95.3%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches 72;
                                                                                             Disclosure; Page 31-32; 47pp; English
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Hashida T,

Hayashi K, Asada K, WPI; 1992-325651/40.

(SOBU/) SOBUE K. (TAKI ) TAKARA SHUZO CO LTD

91JP-00089106 91JP-00358040 92EP-00302591

5-MAR-1992; 29-MAR-1991; 27-DEC-1991;

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C CONA library prepd. from HeLa cells, and the DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence and analysis. Next, the inventors prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide.

C and looked for the functional domain of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide.

C using calmodulin-binding activity and activity as indices activity as indices.

C type I and the form of lower moi. Wt. is called type II. 312AA is a land II. 122AA and type pride that is the C-terminal portion of types II. 312AA is a companied that is the C-terminal portion of types II. 312AA is a sequence of 312AA, and 94AA and 90AA are polypeptides that have a sequence of 116 AAS in the C-terminal contribution of the N-terminal contribution of the N-terminal contribution of the N-terminal contribution and the C-terminal portion. On the N-terminal continued from a PCR primer.

C of 118AA, there are residues Met-Ala Creminal portion. On the N-terminal continued from a PCR primer.

C and on the N-terminal of 90AA, there are residues Met-Ala that also corginated from a PCR primer.

C originated from a PCR primer. On the N-terminal of 122AA and 94AA, there are residues Met-Ala that chain also contains the collypeptide of 116 AAS has both calmodulin-binding activity and activity and ctrivity and have an inhibitory activity. Type I, type II, 312AA, 118AA, 118AA, 116AA all have cropmyosin-binding activity and have an inhibitory activity. Type I, type II, 21AA, 118AA, 
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                                                                                                                                                                                                                                                Caldesmon; calmodulin; actin; binding; actomysin system; regulation; ss
                                                                                                                                                                              Sequence encoding a polypeptide of human caldesmon designated type (heavy) AA.
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                                      AAQ28986 standard; cDNA to mRNA; 1677 BP
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(TAKI ) TAKARA SHUZO CO LTD
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P-PSDB; AAR27363.
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Length 1677;

Score 1086.2; DB 2; Pred. No. 7.6e-244;

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Query Match Best Local Similarity

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29-MAR-1991;
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count clones that encode polypeptide of human caldesmon were selected from a cDNA library prepd. from Hela cells, and the DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis. Next, the inventors prepared polypeptides of various lengths, analysis. Next, the inventoral domain of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide. There are two forms of caldesmon. The form of higher mol. wt. is called type I and the form of lower mol. wt. is called type I and the form of lower mol. wt. is called type II. 312AA and of the contrainal portion of types I and II. 122AA and polypeptide that are in the central portion of 118AA, lacking sequence of 88 AAs that are in the central portion of 118AA, lacking sequence of 88 AAs that are in the central portion of 118AA, lacking collaboration of the N-terminal portion of 118AA, lacking of 118AA, there are residues Met-Ala that also and on the N-terminal of 90AA, there are residues Met-Ala that also criginated from a PCR primer. On the N-terminal of 122AA and 94AA, there are residues Met-Ala that also
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                                    1531 ATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCT
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(TAKI ) TAKARA SHUZO CO LTD
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are residues Met-Ala that originated from PCR primer. The polypeptide (typeI, 192AA, 122AA, 118AA, and 116AA) that contains the polypeptide of Il6 AAs has both calmodulin-binding activity and actin-binding activity. Type I, 1990 II, 312AA, 122AA, 118AA, 116AA all have tropomyosin-binding activity and have an inhibitory activity to actomyosin-binding activity and have an inhibitory activity to accompany as the functional unit of human caldesmon is identified as being 116AA. (Updated on 25-MAR-2003 to correct PA field.)
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count ilbrary prepd. from HeLa cells, and the DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis. Next, the inventors prepared polypeptides of various lengths, analysis. Next, the inventoral operation of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide. There are two forms of caldesmon. The form of higher mol. wt. is called type I and the form of lower mol. wt. is called type II. 312AA and 194A, and 194A and 90AA are polypeptides that have a sequence of 116 Aps in the C-terminal sequence of 88 AAs that are in the central portion of 118AA, lacking both the N-terminal portion and the C-terminal portion. On the N-terminal C of 118AA, there are residues Met-Ala that originated from a PCR primer. Or the N-terminal of 90AA, there are residues Met-Ala that also originated from a PCR primer. On the N-terminal of 122AA and 94AA, there are residues Met-Ala that also
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                                                                                                   1484 GAAACAAGTCACCTGCTCCCAAACCTTCTGACTTGAGACCAGGAGACGTATCCAGCAAGC 1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide(s) with calmodulin- and actin binding activities - useful for treating and diagnosing cancer and regulating digestive tract motility as vasodilators.
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                                                                                                                                       GAAACAAGTCACCTGCTCCCAAACCTTCTGACTTGAGACCAGGAGACGTATCCAGCAAGG
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                                                                                                                                                                                                                                                                                                                                        Sequence encoding a polypeptide of human caldesmon designated 312
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(TAKI ) TAKARA SHUZO CO LTD.
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(first entry)
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27-DEC-1991;
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Pred. No. 5.5e-208;
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Best Local Similarity 99.6%;
Matches 935; Conservative
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The present sequence is one of a large number of 5' ESTs derived from manya encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyak RNAs derived from 30 different tissues. Ests squences usually correspond mainly to the 3' untranalated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with inteact 5' ends and can therefore be used to obtain full length cDNAs and encounted the longer cDNA sequences and encounted from uppartness and chromosome mapping procedures. They are used to obtain uppartness regulatory sequences and to design expression and secretion
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841 CCCAAACCTTCTGACTTGAGACCAGGAGACGTATCCAGCAAGCGGAACCTCTGGGAAAAG 900
                                                                                                                                                                                                                                                                       , expressed sequence tag, secreted protein, cDNA isolation, chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 903; 71pp + Sequence Listing; English
                                    CAATCTGTGGATAAGGTCACTTCCCCCACTAAGGTTTGA 2827
                                                       Giordano J;
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P-PSDB; AAG00899.
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Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung coprostate cancer; ss.
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Obata Y, Pfreundschuh M, Tureci O, Sahin U;
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10-OCT-1997;
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                                                                                                                                                                                The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a mucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product with an agent that specifically product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers.
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Best Local Similarity 97.0%; Pred. No. 4.9e-151;
Matches 733; Conservative 0; Mismatches 20; Indels 3
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New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers.
                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                        human;
lung ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 139 C; 137 G; 212 T; 0 U; 20 Other;
                                                                                                                                                                                                                                          Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                  CCGATCGAAACTCAGAGGAGGAAGAAGAAGAGGA 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.1%; Pred. No. 1.4e-129;
Matches 647; Conservative 0; Mismatches 43;
                                                                         721 CCGATCGGAAACCTTCAAGAGGAGGAAGAAGAAGA 756
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97US-0061599P.
97US-0061765P.
97US-000248705.
97GB-00021697.
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                                                                                                                  RESULT 13
AAX39870/c
ID AAX39870 standard; DNA; 706 BP.
                                                                                                                                                                                                                    Gastric cancer associated gene
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Obata Y,
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                                                                                                                                                                                                                                                                      prostate cancer; ss
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10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 GAAACCCAIGCTGTGAAATANAGACTTTTNTACTGATCATCATAACTCTGTATTTGAGCA
                     2693 CTAAC-TAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCTGACTTGAGACC
                                                                                                                                                                                                                                                                                                                                                       CAGTIGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTGATTTACTAATTGGGTTC
                                                                                                                                                                                                                                                                                                                                                                              395 CAGTIGIANAGGGCTAAITCGCTCTGTTTTGTATTTATGTTGATTTACTAAATTGGGTTC
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2576 AACATCAAGAGTATGTGGGAGAAAGGGAATGTGTTTTCATCCCCCCACTGCAGCAGG----C
                                                                                            575 CTAACTTAAAACCCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTNTGACTTGAGNCC
                                                                                                                                                                                                             2752 AGGAGAC-GTATCCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACTT
                                                                                                                                                                                                                                  CCCCCACTAAGGTTTGAGACAGTTCCAGAAAGAACCCCAAGCTCAAGACGCAGGAGGT
                                                                                                                                                                                                                                                                                                           Human cancer associated gene sequence SEQ ID NO:100.
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us-10-084-817-30.rng

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AAC77607 to AAC78486 encode the human cancer associated proteins given in AAC77607 to AAC4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic, proliferative, vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitherary; immunomodulator; antidiamatory; antilithyroid; antialregic; antibactic; antiasthmatic; antitherary; immunomodulator; carminomodulator; antidiamatory; antiphrorective; cardiant; thrombolytic; coagulant; corresponderation; ansological; antiphrorective; cardiant; thrombolytic; coagulant; coorropic; vasotropic; antippsoriatic and antiangiogenic. The nootropic; vasotropic; antippsoriatic and antiangiogenic. The present invention may be used to reat immune disorders by activating corresponding antibodies; agonists and antagonists from immune cells, polypeptides, antibodies; agonists and ordanned inferentiation of mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate rejection, modulate haemostatic or thrombolytic activity, modulate rejection, modulate haemostatic or thrombolytic activity, modulate agonists and antagonists may be also be used in drug screens. AAC78449 to agonists and antagonists may be also be used in the exemplification of
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                                                                                                                                                                                                                                                                        Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 584.2; DB 3; Length 2511; Pred. No. 3.3e-126; 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2511 BP; 814 A; 445 C; 443 G; 803 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 690-691; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.7%;
Matches 589; Conservative
                                                       08-MAR-2000; 2000WO-US005882
                                                                                              99US-0124270P
                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                              Ruben SM;
                                                                                                                                                                                                                  2000-587533/55
                                                                                                                                                                                                                                      P-PSDB; AAB43497
                                                                                              12-MAR-1999;
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ANH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to expression by rectifying mutations or deletions in a patient's genome to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 time of publication, meaning no sequences are present for SEQ ID NO:1027 3183 AGABABATGAACCGTAGTTTTTGTTTTTTABATACAGAAGTCATGTTGTTTTTGACTT 3242 TATAATAAAGCATGGAAGAAATTATCTTAGTAGGCAATTGTAACACTTTTTGAAAGTAAC 3302 493 AGAAAAATGAACCGTAGTTTTTTTTTTTTAATACAGAAGTCATGTTGTTTCTGCACTT 552 433 ACATCTGAAGTCAACAGAAGATCCAAGTTTAAAATTGCCTGCGGAATGTGTGCAGTATCT 492 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers. Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 7; ss. Sequence 2511 BP; 814 A; 445 C; 443 G; 803 T; 0 U; 6 Other; Human colon cancer antigen encoding cDNA SEQ ID NO:173. Rosen CA Claim 1; Page 2329-2330; 9803pp; English Birse CE, BP AAH33117 standard; cDNA; 2511 99US-0157137P. 99US-0163280P. 28-SEP-2000; 2000WO-US026524. (HUMA-) HUMAN GENOME SCI INC (first entry) Ruben SM, Barash SC, WPI; 2001-235357/24. P-PSDB; AAG73686. WO200122920-A2. 29-SEP-1999; 03-NOV-1999; Homo sapiens 03-SEP-2001 05-APR-2001 AAH33117; 553 3243 613 RESULT 15 AAH33117 요 ò 셤 ò 셤 8

DB 4; Length 2511;

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15.8%;

Query Match

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	ATAAGG	ATAAGO	GCAGG	GCAGG	TAAAT	TAAAT	TATAT	TATAT	SCCTGT	sccrer	TGTAT	TGTAT	GCCTGC	recere	PAGAAG	SAGAAG	AATTGT	ATTGT	TTAAATI	crrraa
3.3e-126 hes 8	CTGTGG	CTGTGG	CAAGAC	CAAGAC	ATTTA	ATTA	TATCAC	TATCAC	CAGGAC	CAGGAG	TAACTO	TAACTO	TAAAAT	AAAAT	PAPATAC	PAPATA	CTTAGTAGGCAATTGTAACA	TAGGC	BGTTGC	Ē
d. No. 3.3 Mismatches	CCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGATAAGGT	AGCAAT	CAAGCT	CAAGCT	PATGTTO	ATGTT	GTATA	CCAGTAAACCCATGTATATTATCACTATATT	TTTGC	rrrec	GTGAAATAGAGACTTTTCTACTGATCATCATAACT	ATCATC	CAAGTT	CAAGTT	PTTTT.	ratara	ATCTTA	TATAATAAAGCATGGAAGAAATTATCTTAGTAGGCAATT	SATAAT(	crecaaraaree
Pred.	GGGAAA	GGGAAA	AGAACC	AGAACC	GTATT	GTATT	ACCCAT	ACCCA	PACTGC	PACTGC	CTACTG	TACTG	AAGATC	AGATO	AGAAAATGAACCGTAGTTTTTGTTT	rrrrg	TATAATAAAGCATGGAAGAAATTAT	BAAATT	TACTGC	racido
98.7%; ive	ACCTCT	ACCTC	CCAGA	CCAGAZ		TGTTT	CAGTA	CAGTA	PAAAAG	AAAAG	CTTTTC	CTTTT	AACAG	PACAG	CGTAG	CGTAG	ATGGAA(	ATGGAA	TTGAAA	rtgaaata
larity 98. Conservative	AGCGGA	AGCGGA	ACAGTI	ACAGTI	TCGCTC	TCGCTC	ATATCO		CATGGI	CATGG	TAGAGA	TAGAGA	GAAGTO	GAAGTO	ATGAAC	ATGAAC	AAAGC	AAAGC	CAGAT	CAGATT
겉	CAGCA	GAGCA	TTTGAG	TTGAG	GCTAATTCGCTCTGTTT	GCTAAT	TTTTCA	TTTCAATATC	GATGTT	GATGTT	GTGAAA	GTGAAATAGAGA	ACATCT	ACATOT	AGAAAA	AGAAAA	TATAAT	TATAAT	CCATTI	CCALTI
	2763	73	2823	133	2883 (	193 (	2943	253	3003 (	313 (	3063	373 (	3123	433	3183	493	3243	553	3303	613
Best Local Matches 58				٠																
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Search completed: March 10, 2004, 11:00:07 Job time : 916.994 secs Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence

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ALIGNMENTS

Sequence Sequence Sequence

Sequence Sequence

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Sequence 14, Application US/08285440
Patent No. 5532337
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Wanhington
STATE: D.C.
COUNTY: U.S.A.
STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,440
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION TO 1992
ATTOM APPLICATION DATA:
APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTOMNEY/AGENT INFORMATION:
NAME: WARTEN WARE: MATCH JF.
REGISTRATION NUMBER: 33,367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2215 base pairs
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RANT-SENSE:
FRANCESES:
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ORIGINAL SOURCE: Human
ORGANISM:
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STRANDEDNESS:
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              March 10, 2004, 09:19:42 ; Search time 169.055 Seconds
(without alignments)
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-630-3449-113
US-08-630-3449-113
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US-08-630-3449-112
US-08-630-3449-110
US-08-285-4440-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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3702
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TGTTTCTAAAGAAACCCATGCTGTGAAATAGAGACTTTTCTACTGATCATCATAACTCTG 1958
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                                                                                                                                                           1002 GAGGAACTCAAGAAAAAGAAGGAGGAGGAGAAAGGAAGGTCCTGGAGGAGGAAGAGAGGAGG
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                                 882 GGGGCCCCCAGGTGGAAGCCGGCAAAAGGCTGGAGGAGCTTCGTCGTCGTCGCGGGGAG
                                                                 2081 ACCGAGAGCGAAGAGTTCGAGAAGCTCAAACAGAAGCAGCAGGAGGCGGCTTTGGAGCTG
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IMMEDIATE SOURCE: Hela Cell
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FEATURE:
NAME/KEY:
IOCATION: 12-1685
IDENTIFICATION METHOD:
OTHER INFORMATION: Molecular weight"
FEATURE:
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IOCATION: 2103-2108
IDENTIFICATION METHOD:
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IOCATION: 2103-2108
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "poly A signal"
FEATURE:
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IOCATION: 7009-2015
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "poly A site"
PUBLICATION INFORMATION:
AUTHORS:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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DATE:
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Best Local Similarity 94.5%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches
                                                ; LOCATION: 2099-2215
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OTHER INFORMATION: molecular weight"
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US-08-630-349-14
US-08-630-349-14
Sequence 14, Application US/08630349
Patent No. 573908
GENERAL INFORMATION:
PAPPLICANT: Ken'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STRYE: D.C.
COUNTRY: U.S.A.
ZIP: 20065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: Diskette, 3.5 inch, 144 mb
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COMPUTER: Diskette, 3.5 inch, 140
SPELING DATE: April 10, 1996
CLASSIFICATION NUMBER: 08/285,440
FILING DATE: April 10, 1996
CLASSIFICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY PORTOR INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
INFORMATION FOR SEQ ID No: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE: Human
IMMEDIATE SOURCE: Hela Cell
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LOCATION: 2103-2108
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                      462 CAAGAAAGATACGAGATAGAGGAAACAGAAACAGTCACCAAGTCTACCAGAAGAATGAT
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FEATURE:
NAME/KEY:
LOCATION: 12-1607
LOCATION: 12-1607
LDBWIFICATION METHOD:
OTHER INFORMATION: /note= "human caldesmon of lower OTHER INFORMATION: molecular weight"
FEATURE:
NAME/KEY:
LOCATION: 2025-2030
LDENTIFICATION METHOD:
OTHER INFORMATION: /note= "poly A signal"
FEATURE:
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LOCATION: 2121-2137
LOCATION METHOD:
LIBERIFICATION METHOD:
OTHER INFORMATION: /note= "poly A site"
AUTHORS:
                    ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 50
COMPUTER: IBM Compatible
OPERATING SYSTEM: Ms.-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,440
FILING DATE:
APPLICATION STARM
RECASTRICATION: 27, 1992
ATTORNEY/AGBNT INFORMATION:
NAME: Warren M. Cheek, Ur.
RECASTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER: 33,367
REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX:
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGHT: 213 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: linear
MOLECULE TYPE: cDNA tO mRNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOUNCE: Human
ORGANISM:
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STRAIN:
INDIVIDIAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: Hela Cell
LIBRARY:
CLONE:
POSITION IN GENOME:
CHOMOSOME/SEGMENT:
MAP POSITION:
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     COUNTRY:
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                                                                                                                       1422 GCTGAAGGTGTACGCAACATCAAGAGTATGTGGGAGAAAGGGAATGTGTTTTCATCCCC
                                                                                                                                                                                                                                                                       ATCAATGAATGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCT
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                                                                              2561 GCTGAAGGTGTACGCAACATCAAGAGTATGTGGGAGAAAGGGAATGTGTTTTCATCCCCC
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Fatent No. 5532337
GENERAL INFORMATION:
APPLICANT: Ken'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CORRESPONDENCE ADDRESS:
STREET: 805 Fifteenth Street, N.W., #700
STATE: D.C.
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                                                                                                                                                                                                                                                                                GAGAATTCATGACCCACAAACTTAAACATACTGAGAATACTTTCAGCCGCCCTGGAGGA
                                                                                                                                                                                                                                                                                                                       775 GGGCCAGCGTGGACACCAAGGAGGCTGAGGGGGCCCCCCCAGGTGGAAGCCGGCAAAAGGC
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                                                                                           Gaps
                                                                                           4;
                                                                    DB 1; Length 2137;
                                                                                           54; Indels
                                                                  Query Match 40.0%; Score 1481.6;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1548; Conservative 0; Mismatches
        FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
DOCUMENT NUMBER:
                                            S-08-285-440-13
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Patent No. 5739008;
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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1375 GGGAGAAAGGGAATGTGTTTTCATCCCCACTGCAGCAGGCACACCAAATAAGGAAACTG
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LOCATION: 12-1607
LOCATION: 12-1607
LOCATION METHOD:
OTHER INFORMATION: molecular weight"
FEATURE:
LOCATION: 2025-2030
LOCATION: 2025-2030
LDEWNIFICATION METHOD:
OTHER INFORMATION: /note= "poly A signal"
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
1 LOCATION: 2121-2137
1 IDENTIFICATION METHOD:
2 OTHER INFORMATION: /note= "poly A site"
US-08-630-349-13
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE: Human
IMMEDIATE SOURCE: Human
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GENERAL INFORMATION

PAPELICANT: Ken'ichic HAYASHI et al.

TITLE OF INVENTION: POLYPEPTIDE

NUMBER OF SEQUENCES: IN WARD STREET: BOS FILEERTH STREET, N.W., #700

STATE: 20005

CONDITION: Washington Street, N.W., #700

STATE: 0.0

CONDITION: Washington Street, N.W., #700

STATE: 0.0

CONDITION: Washington Street, S. 25 inch, 500 kb

COMPUTER: Day Compared: Day Street, S. 25 inch, 500 kb

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        1531 ATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCT 1590
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                                                                                       2741 GACTTGAGACCAGGAGACGTATCCAGCAAAAGCGAACCTCTGGGAAAAGCAATCTGTGGAT
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Patent No. 553237

GENERAL INFORMATION:

APPLICANT: Ren'ichiro HAYASHI et al.

APPLICANT: Ren'ichiro HAYASHI et al.

TITE OF INVENTION:

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wendercth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATION TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATION SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION NDATA:

APPLICATION NUMBER: US/08/285,440

FILING DATE: March 27, 1992

ATTORNEY APPLICATION NUMBER: 33,367

FILING DATE: March 27, 1992

ATTORNEY MARTEN M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                       1651 AAGGTCACTTCCCCCACTAAGGTTTGA 1677
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LENGTH: 1599 base pairs
TYPE: uncleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL:
ANTI-SENSE:
FRACKENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
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1244 ACAGCAGACTGGAGCAGTATACCAGTGCAATTGAGGGAACAAAAAGCGCAAAACCTACAA 1303
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Pred. No. 6.8e-234;
0; Mismatches 48; Indels
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| Sequence 11, Application US/08630349
| Patent No. 5739008
| GENERAL INFORMATION:
| APPLICANT Ken'ichiro HAYASHI et al. |
| TITLE OF INVERTION: POLYPEPTIDE |
| NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: ADDRESSE: Wenderch, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STREET: B.C. |
| CITY: Washington STREET: B.C. |
| STREET: B.C. |
| COUNTRY: U.S.A. |
| STREET: B.C. |
| COMPUTER: IDEN COMPATIBLE FORM: MSD1UM TYPE: Diskette, 3.5 inch, 144 mb COMPUTER: ISM COMPATIBLE PORM: MS-D0S SOFTWARE: Wordperfect 5.1 |
| COMPUTER: IDEN COMPATIBLE |
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| COMPUTER: IDEN COMPATIBLE |
| CONFORTION NUMBER: US/08630,349 |
| FILING DATE: APPLICATION NUMBER: 07/858,947 |
| FILING APPLICATION NUMBER: 07/858,947 |
| FILING APPLICATION NUMBER: 07/858,947 |
| FILING APPLICATION NUMBER: 07/858,01 |
| ATTORNATION FOR SEQ IND NO: 11: SEQUENCE CHARACTERISTICS: |
| LENGTH: 1.1599 base pairs
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ORIGINAL SOURCE: Human
; IMMEDIATE SOURCE: Hela Cell
US-08-630-349-11
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Best Local Similarity 95.5%;
Matches 1028; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                         1812 CTACCTTCAAAAAGGAAGGATCAAAGATGAAAGGTTAAAAAGGACAAAGGACCCAAAG
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Sequence 10, Application US/08285440
Patent No. 523237
GENERAL INFORMATION:
APPLICATIVE: Ken'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYBETIDE
NUMBER OF SEQUENCES: 32
COUNTY: Washington
STATT: D.C.
TITLE OF INVENTION: POLYBETIDE
COUNTY: Washington
STATT: D.C.
TITLE: 20005
TITY: Washington
STATT: D.C.
TITLE: 20005
TITLE: 20005
TITLE: D.C.
TOWPUTER READABLE FORM:
WENDIUM TYPE: Diekette, S.25 inch, 500 kb
OCHOPHORY READABLE FORM:
WENDIUM TYPE: Diekette, S.25 inch, 500 kb
OCHOPHORY READABLE FORM:
WENDIUM TYPE: Diekette, S.25 inch, 500 kb
OCHOPHORY READABLE FORM:
WENDIUM TYPE: Diekette, S.25 inch, 500 kb
OCHOPHORY READABLE FORM:
APPLICATION NUMBER: US/08/285,440
TILLING DATE: MARCH IN TOPERATION:
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                                                                          Query Match 25.3%; Score 937.4; DB 1; Best Local Similarity 99.9%; Pred. No. 6.1e-219; Matches 938; Conservative 0; Mismatches 1;
           FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
DOCUMENT NUMBER:
                                       ;
US-08-285-440-10
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                            361 AGGAGGCTAAAGGAAGAAGAGATTGAAAGGCGAAAGAGCAGAAGCTGCTGAGAAACGCCAGAAG
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Sequence 295, Application US/09385982

Betent No. 626234

GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
GURRENT FILING DATE: 1999-06-30

BARLIER FILING DATE: 1999-06-08

BARLIER FILING DATE: 1999-01-27

BARLIER FILING DATE: 1999-01-27

BARLIER FILING DATE: 1998-01-27

BARLIER FILING DATE: 1998-01-31

NUMBER OF SEQ ID NOS: 544

SOFTWARE: FESSERE FOR Windows Version 3.0

SEQ ID NO 295

LENGTH: 606
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96.5%; Pred. No. 6.1e-95;
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NAMEKEY: misc feature
LOCATION: (1)...(606)
OTHER INFORMATION: n =
US-09-385-982-295
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-385-982-295/c
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                                                            Sequence 10, Application US/08630349
Parent No. 573908
GENERAL INPORMATION:
TITLE OF INVENTION: POLYPEFILDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 20005
COMPUTER READABLE FORM:
MUDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOUTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,349
FILING DATE: April 10, 1996
CLASSIEDRATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,440
FILING DATE: Abquet 4, 1994
PRIOR APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warten M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 939 base pairs
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STRANDEDNESS: double
TOPOLOGY: line-
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DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-285-440-9
                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
CRELL LINE:
CREANELLE:
INMEDIATE SOURCE: Hela Cell
LIBRARY:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
MAP POSITION:
UNITS:
CRANURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION:
MATHORS:
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                    STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA to MYPOTHETICAL: ANTI-SENSE: PRAGNENT TYPE: ORIGINAL SOURCE: Human ORGANISM:
nucleic acid
                                                                                                                                                                                                                                                                                   STRAIN:
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                                                                 2570 GTACGCAACATCAAGAGTATGTGGAAAAAGGAATGTGTTTTCATCCCCCACTGCAGCA 2629
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                                                                                                                           457 GTACGCAACATCCAAGAGTATGTGGNAGAAGGAATGTGTTTTCATCCCCCANTGCAGCA
      0; Gaps
      16; Indels
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APPLICANT: Ken'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wanderoth, Lind & Ponack
STREET: BOS Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COMPITY: U.S.A.
ZIP: 20005
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION NUMBER: US/08/285,440
FILING DATE:
RELING DATE:
PILING DATE:
PRILING DATE:
RESISTATION NUMBER: 07/858,947
PILING DATE:
REGISTATION NUMBER: 33,367
PRISEPENMENT INFORMATION:
NAMM: WALTEN M.CHOEK, JT.
REGISTATION NUMBER: 33,367
PREFERENMENTENDUMERT 33,367
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      0; Mismatches
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Patent No. 5532337
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SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
      Matches 437; Conservative
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2474 AGCAGACTGGAGCAGTATACCAGTGCAATTGAGGGAACAAAAAGCGCAAAACCTACAAAG 2533
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  DB 1; Length 369;
                                                       2; Indels
Query Match

9.5%; Score 350.8; DB 1
Best Local Similarity 99.4%; Pred. No. 4.4e-76;
Matches 352; Conservative 0; Mismatches 2
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US-08-28-440.49

J Sequence 8, Application US/08285440

Patent No. 553237

GENERAL INFORMATION:
GENERAL INFORMATION:
FITLE OF INVENTION:
FOLVESTIDE
NUMBER OF SEQUENCES:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CTTY: Washington
STATE: D.C.
COUNTY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Diskette, S.25 inch, 500 kb
SOFTWARE: DisplayWitte
CURRENT APPLICATION DATA:
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/ACRIT INROPMATION:
NAME: Warren M. Check, Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL INE:
ORGANELLE:
IMMEDIATE SOURCE: Hela Cell
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LDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE: Human
ORGANISM:
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POSITION IN GENOME:
CHROMOSONE/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
NAME/KEY:
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  316 AACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACT
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MOLECULE TYPE: CDNA tO MRNA
MOLECULE TYPE: Human
IMMEDIATE SOURCE: Hela Cell
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RESULT 14

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Search completed: March 11, 2004, 14:41:48 Job time : 173.055 secs
STRANDEDNESS:
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                                                                                                                                    DB 1; Length 357;
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                                                                                                                                    Query Match 9.5%; Score 350.4; DB 1
Best Local Similarity 99.7%; Pred. No. 5.4e-76;
Matches 351; Conservative 0; Mismatches 1
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COMPUTER: Diskette, 3.5 inch, 144 mb
OPERATING SYSTEM: MS-DOS
SOOTWARE: WOORDerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,349
FILING DATE: April 10, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/285,440
FILING DATE: Aquet 4, 1994
FILING DATE: Aquet 4, 1994
FILING DATE: March 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTATION NUMBER: 33,367
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08630349
Patent No. 5739008
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
); DATE:

) DOCUMENT NUMBER:

); FILING DATE:

; PUBLICATION DATE:

) RELEVANT RESIDUES IN SEQ ID NO:

US-08-285-440-8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                      Length 357;
                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                   Query Match 9.5%; Score 350.4; DB 1; Best Local Similarity 99.7%; Pred. No. 5.4e-76; Matches 351; Conservative 0; Mismatches 1;
TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE: Human

MEDIATE SOURCE: Hela Cell
US-08-630-349-8
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Sequence 1194, Ap Sequence 1194, Ap Sequence 1028, Ap Sequence 2028, Ap Sequence 255, App Sequence 2512, Ap Sequence 571, Ap Sequence 5761, Ap Sequence 50761, Ap Sequence 50761, App Sequence 2159, App Sequence 11790, App Sequence 11790, App Sequence 11790, App Sequence 11790, App Sequence 11, Appl S

Sequence 1966, A Sequence 20462,

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61 CATTGGCTGCCTATTAGAAAACGACAGGACAATGCATACCACCGCCTCCCGACTGTAAA
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; OTHER INFORMATION: Incyte ID No. US20030119009A1 1312325CB1
US-10-084-817-30
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APPLICANT: Sharon E. Plon
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
FILE REFERENCE: PA-0046 US
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SEQ ID NO 30
LENGTH: 3702
                  14 US-10-060-036-11944

10 US-09-918-995-19285

10 US-09-918-995-19285

14 US-09-871-161-298

15 US-09-25-301-68

16 US-09-25-301-68

17 US-09-25-301-68

17 US-09-955-301-68

17 US-09-955-301-68

17 US-09-956-355-37

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3702; Conservative 0; Mismatches
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Publication No. US20030119009A1
GENERAL INFORMATION:
                                TYPE: DNA ORGANISM: Homo sapiens
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Sequence 1815, Ap
Sequence 121, App
Sequence 721, App
Sequence 31, Appl
Sequence 31, Appl
Sequence 116, App
Sequence 136, App
Sequence 215, App
Sequence 22, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
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                                                                                                                                                March 11, 2004, 03:37:21 ; Search time 862.637 Seconds
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15799.545 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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US-09-873-367C-721

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US-09-873-367C-721

US-01-062-674-1817

US-01-084-817-31

5 US-10-084-817-31

5 US-10-341-434-215

US-09-765-231A-215

US-09-765-231A-215

US-09-765-301-100

US-09-925-301-100

US-09-974-298-183

US-09-925-301-100

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DB 14; Length 3702;

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Sequence 2406, Application US/09880107

Sequence 2406, Application US/09880107

Sequence 2406, Application US/09880107

Sequence 2406, Application

Batelicant: No. US20020142981A1

APPLICANT: Horne, Darci T.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-2508-W0

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2406

LENGTH: 3610

TYPE: DNA
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GAAAGAAGACAAGGAAAAAGGAGGAGGAAGAAGAGAAAAAGAGCCAAAAGCGAGGGAGCATTGG 1056 AGAAAATCAGGTAGAGGTGATGGTGGAAGAGAAAACAACTGAAAGCCAGGAGGAAACAGT 1116 900 780 360 CCAGGTGGAGGTGAATGCCCAGAACAGTGTGCCTGACGAGGAGGCCCAAGGACAACCACCAC 480 756 540 600 840 240 636 420 816 660 936 720 966 336 120 456 516 300 AATAACAGATGCAAGTCTGCCTCCCAAGCAGAAGAATGCAAAATGACACAGCAGAAAA 876 9 AACAGAAACAGTCACCAAGTCCTACCAGAAGAATGATTGGAGGGATGCTGAAGAAAACAA 181 GCTGACCTGTCCAGACATCATCTGGTCTCCCTGAACCTGAAATCACACCATGGATGATTT AGCCGACAGGACGGCTGCGGCAGAGGAGGAGGAGAAGCATCCTTGGGACAGGTGACGG AAACACTCAAGTGGAAGGGGATGATGAGGCCGCATTCCTGGAGCGCCCTGGCTCGGCGTGA AAACACTCAAGTGGAAGGGGATGATGAGGCCCATTCCTGGAGCGCCCTGGCTCGGCGTGA 541 GGAAAGACGCCAAAAAAGGCCTTCAGGAGGCTCTGGAGGGGCAGAAGGAGTTCGACCAAC AACAGAAACAGTCACCAAGTCCTACCAGAAGAATGATTGGAGGGGATGCTGAAGAAAACAA 1 ccidcorcoccidciidcictorcoccidcorcoccidorinaagaaarcagicocrio TITCCGACTIAGICCICGGGAAGAAGTITCAGACTACAAGGTATCATTGGAACATTTCAA 61 TITCCGACITAGICCTCGGGAAGAAGITTCAGACTACAAGGTAICAITGGAACATITCAA GATCATCAAATTCCACAGGGATTGGTGACCAACCAGAAGGCTCAGACTCTGATT GATCATCAAATCAAATTCCACAGGATTGGTGACCAACCAGAGGCTCAGACTT TGAGCGTCGCAGAGCATAGAAGGCAAAAGAGGAGGAGGAGGAGCGACTCGAAGCAGAAAG TGAGCGTCGCAGAGAACTTAGAAGGCAAAAGAGGGAGGAGAATGCGACTCGAAGCAGAAAG AATCGCCTACCAGAGGAATGACGATGATGAAGAGGAGGCAGCCCGGGAACGGCGCCGCCG AATCGCCTACCAGAGGAATGACGATGATGAAGAGGAGGCAGCCGGGGAACGCCGCCGCCG CCAGGTGGAGGTGAATGCCCAGAACAGTGTGCCTGACGAGGAGGCCAAGACAACACCAC GGAAAGACGCCAAAAACGCCTTCAGGAGCTCTGGAGCGGCAGAAGGAGTTCGACCCAAC 217 CCTGCCTGCCTGCTTGCTCTGGCTGTGCTCCTGCTTAAAGAAATCAGTCCTTCC GCTGACCTGTCCAGACATCATCTGGTCTCCCTGAACCTGAAATCACACCATGGATTTT AGCCCCACAGGAACGGCTGCGGCAGAAGCAGGAGGAAGAATCCTTGGGACAGGTGACCGA Length 3610; ä , OTHER INFORMATION: Genbank Accession No. US20020142981A1 M83216 US-09-880-107-2406 21; Indels DB 9; Score 3116.4; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 99.3%;
Matches 3140; Conservative ( ORGANISM: Homo sapiens FEATURE: 877 781 277 337 121 241 517 301 361 421 697 757 817 601 661 937 721 997 1057 841 1117 901 397 457 577 637 481 ď 셤 8 8 셤 셤 윉 ઠે d ò g ઇ . <del>Q</del> ઠે 엄 ઠે 셤 ò g ò g δ ઠે 셤 ઠે ઠે ò ઠે ઠે 셤

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                                                                                                          GENERAL INFORMATION:

APPLICANT: Soppet, Daniel
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Mena
APPLICANT: Endress, Mena
APPLICANT: Ener, Reinhard
APPLICANT: Ener, Reinhard
APPLICANT: Carter, Renneth
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 699290-64
CURRENT PLILIGATION NUMBER: U.S. 60/236,891
PRIOR PELICATION NUMBER: U.S. 60/236
PRIOR PELICATION NUMBER: U.S. 60/236,842
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: Patentin version 3.0
LENGTH: 3810
LENGTH: 3810
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Pred. No. 0;
0; Mismatches 21; Indels
TCTTTAAAAAAAAAAGAATGTACTGTTAAGGTATTACTTTT 3161
                                                                     Sequence 721, Application US/09873367C Publication No. US20030165839A1 GENERAL INFORMATION:
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Best Local Similarity 99.3%;
Matches 3140; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: unsure

! LOCATION: (1) ... (4566)

! OTHER INFORMATION: a, t, c, g, or other

US-10-062-674-1817
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ORGANISM: Homo sapiens
FEATURE:
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2641 ACGCAGGACGAGGGTTGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTGATTT
2641 ACGCAGGACGAGGACCAGTTGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTGATTT
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               1621 AGATGAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCG
                                                                                                                                1801 TGAGGGGCCCCCCAGGTGGAAGCCGGCAAAGCTGGAGGAGCTTCGTCGTCGTCGCGGG
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                                                 AAAGAAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAA
                                                                              1957 ACATACTGAGAATACTTTCAGCCGCCTGGAGGGAGGGCCAGCGTGGACACCAAGGAGGC
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                                                                                                                         Sequence 1817, Application US/10062674
Sequence 1817, Application US/10062674
Publication No. US20040005559A1
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
FILE REFRENCE: PA-0026-1 CIP
CURRENT APPLICATION NUMBER: US/10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: US 09/625,102
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SOFTWARE: PERL PROGram
SEQ ID NO 1817
LENGTH: 4566
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OTHER INFORMATION: Incyte ID No. US2004000559A1 256147.58c
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63.6%; Score 2353; D
Best Local Similarity 92.0%; Pred. No. 0;
Matches 2616; Conservative 0; Mismatches
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               GACGCAGGACGAGCTCAGTTGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTGATT 2915
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OTHER INFORMATION: Incyte ID No. US20020156263A1 022404.25
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Best Local Similarity 76.9%; Pred. No. 0;
Matches 2585; Conservative 0; Mismatches
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US-09-974-298-36
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1739 1740 TCCTAAAGAAACAGGGAGAAGAAGGGAACTAAAGTGCAAGCTAAAAGAGAAAAGCTCC 1799 1079 1148 1619 1019 1103 1080 TGGAAGAGAAAACAACTGAAAGCCAGGAGAAACAGTGGTAATGTCATTAAAAATGGGC 1139 1140 AGATCAGTTCAGAAGAGCCTAAACAAGAGAAGGAGGGAACAAGGTTCAGATGAGATTT 1199 1200 CCCATCATGAAAAGATGGAAGAAGAAGAAAAAAAAGAGCTGAGGCAGAGAGGCAAAGGT 1259 1260 TGGAAGCAGAAGAAAGAAATTAAAGCCGAGCAAGACAAAAAAGATAGCAGATGAAC 1319 1440 AGGAGGAAGAAAAGGGCAGCAGAGGAGAGGCAGAGGATAAAGGAGGAAGAGAAAAAGGG 1499 1500 CAGCAGAGGAGGCAGAGATAAAAGAGAAAAAGAGAAAAAGGGCAGCAGCAGAGGAGGCAAA 1559 1620 TAGAAGAGAAAAAACATGCCATGCAAGAGACAAAGATAAAAGGGGGAAAAGGTAGAACAGA 1679 1043 179 923 983 959 863 1560 GGGCCAGGGCAGAGGAGGAAGAAGGCTAAGGTAGAAGAGCAGAAACGTAACAAGCAGC 1680 AAATAGAAGGGAAATGGGTAAATGAAAAGAAAGCACAAGAAGATAAACTTCAGACAGCTG 1044 ACCAGAAGAATGATTGGAGGGATGCTGAAGAAAAGAAGAAGAAGAAGAAGAAGAAAGGAGG 1020 AGGAGGAAGAGGAGAAAGCCAAAGCGAGGAGCATTGGAGAAAAATCAGGTAGAGGTGATGG AAAGTGAAAAGTCGCCAAGAAAGATACGAGATAGAGGAAACAGAAACAGTCACTT 804 Archedccccarrccreanceccreacreacercaseananaecccananaecccrrc AGGAGGCTCTGGAGGGGGAGAGGAGGTTCGACCCAACAATAACAGATGCAAGTCTGTCGC TCCCAAGCAGAAGAATGCAAAATGACACAGAAAATGAAACTACCGAGAAGAAA 984 AAAGTGAAAAGCGAAGAAAGATACGAGATAGAGGAAACAGAAACAGTCACCAAGTCCT 1149 1149 1149 1149 720 780 840 900 096 1149 1149 1149 ద දි දි 상 원 ⋧ g ò ठ क्ष ठ 8 % ద 유 8 G ò නි සි ያ ያ a ઠે 셤 δ 6 B g 8 % ò à g

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Publication No. US200400055591

GENERAL INFORMATION

APPLICANT: LOCING, Jeanne F.; Kaser, Matthew R.

TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS

FILE REPRESENCE: PA-0026-1 CIP

CURRENT APPLICATION NUMBER: US/10/062,674

CURRENT PILING DATE: 2002-01-30

PRIOR PILING DATE: 2000-07-24

NUMBER OF SEQ ID NOS: 2217

SOFURARE: PERL PROGRAM

SEQ ID NO 1816

LENGTH: 4261
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47.8%; Score 1771; DB 15; Length 4261;
Best Local Similarity 76.7%; Pred. No. 0;
Matches 2578; Conservative 0; Mismatches 16; Indels 768; Gaps
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ORGANISH: Homo sapiens
PRATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040005559A1 256147.57
OTHER INFORMATION: 4261)
LOCATION: (1) ... (4261)
CHER INFORMATION: a, t, c, g, or other
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TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REPERENCE: 90 204 208 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Version 3.1
SEQ ID NO 136
LENGTH: 2845 Length 2845; Indels 0; Mismatches 20; DB 15; Score 1578; Pred. No. 0; Sequence 136, Application US/10341434 Publication No. US20030215835A1 GENERAL INFORMATION: Query Match
Best Local Similarity 75.1%;
Matches 2376; Conservative ; NAME/KEY: CDS ; LOCATION: (230)..(1843) ; OTHER INFORMATION: US-10-341-434-136 ORGANISM: Homo sapiens

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1057 AGAAAATCAGGTAGAGGTGATGGTGGAAGAAAAACAACTGAAAGCCAGGAGGAAACAGT 1116 GGTAATGTCATTAAAAATGGGCAGATCAGTTCAGAAGAGCCTAAAACAAGAGGAGAGAG 1176 1177 GGAACAAGGTTCAGATGAGATTTCCCATCATGAAAAGATGGAAGAGGAAGACAAGGAAAG 1236 197 AGACAAAAAGATAGCAGATGAACGAGCAAGAATTGAAGCAGAAGAAAAAGCAGCTGCCCA 1356 GATAAAGGAGGAAGAAAAGGGCAGCAGCAGAGGAGGAGGATAAAAGAGAAGAGAA 1536 1357 AGAAAGAGAAAGGAGAGAGGCAGAAGAGGGGAAAGGGATGAGGGAAGAGAAAAAGGGC 1416 840 848 480 540 720 848 848 360 636 420 969 756 816 900 660 936 966 AATAACAGATGCAAGTCTGCGCTCCCAAGCAGAATGCAAAATGACACAGCAGAAAA 876 <u> AGCCCGACAGGAACGGCTGCGGCAGAAGCAGGAAGAAGAATCCTTGGGACAGGTGACCGA</u> AGCCCGACAGGAACGCCTGCGGCAGAAGCAGGAAGAATCCTTGGGACAGGTGACCGA CCAGGTGGAGGTGAATGCCCAGAACAGTGTGCCTGACGAGGAGGGCCAAGACACACCACAC GGAAAGACGCCAAAAACGCCTTCAGGAGGCTCTGGAGGGGCAGAAGGAGTTCGACCCAAC <u>AACAGAAACAGTCACCAAGTCCTACCAGAAGAATGATTGGAGGGATGCTGAAGAAAACAA</u> AATCGCCTACCAGAGGAATGACGATGATGAAGAGGAGGCAGCCCGGGAACGCCGCCGCCG AAACACTCAAGTGGAAGGGGATGAGGCCGCATTCCTGGAGCGCCTGGCTCGGCGTGA 

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0y 2377 TITCHANTOMATAGCTAACTAAAACCCCAAATGGAAACAACTGCTCCCCAAACC 2736  1366 CCGCATCAATGAATGGCTAACTAAAACCCCAAATGGAAACAACTGCTCTCTCCCCAAACC 1755  136 CTGCATCAATGAACCAACACAAACCCCAAACAACAACAAAAAACCAAAAACAATTCCAAAAAA	RESULT 11 US-09-765-231A-32  i Sequence 32, Application US/09765231A  patent No. US20020119452A1  j Betent No. US20020119452A1  j APPLICANT: Searle/Monsanto  APPLICANT: Phippard, Deborah  APPLICANT: Vasanthakamur, Geetha  APPLICANT: Vasanthakamur, Geetha  APPLICANT: Vasanthakamur, Geetha  APPLICANT: Vasanthakamur, Geetha  APPLICANT: Vasanthakamur, Geetha  APPLICANT: Wa. Xiao-Uun  TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,  TITLE OF INVENTION: Vectors, and cells  FILE REFERENCE: SO-3221 PR  CURRENT APPLICATION NUMBER: US/09/765,231A  CURRENT PILING DATE: 2001-01-18  NUMBER OF SEQ ID NOS: 82  SEQ ID NO 32  LENGTH: 3342  TYPE: DNA  ORGANISM: Homo sapiens  US-09-765-231A-32  Query Match  39.3%; Score 1455.8; DB 9; Length 3342;
1597   AGAGCAGAAACGTAACAAGAGAAAAAAACGCCATGCAAGAACAAAACCCAGAAAAAACCCAGAAAAAACCCAGAAAAAA	

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Patent No. US20020052308A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: PA106

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE PATENTION VOICE: 1099-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE PATENTION VOICE: 1099-03-12

LENGTH: 2511
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LOCATION: (12)
OTHER INPORMATION: n equals a,t,g, on
NAME/KEY: misc_feature
LOCATION: (28)
OTHER INPORMATION: n equals a,t,g, on
NAME/KEY: misc_feature
LOCATION: (44)
OTHER INPORMATION: n equals a,t,g, on
NAME/KEY: misc_feature
LOCATION: (2456)
OTHER INPORMATION: n equals a,t,g, on
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LOCATION: (2456)
OTHER INPORMATION: n equals a,t,g, on
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LOCATION: (2488)
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LOCATION: (2488)
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LOCATION: (2511)
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                                                                            GAAGAAGTTAAGAGCTTCATGGATCGAAAGAAGGGATTTACAGAAGTTAAGTCGCAGAAT
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                      2; Gaps
                    7; Indels
 Pred. No. 0;
0; Mismatches
 Best Local Similarity 99.4%;
Matches 1482; Conservative
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; Squence 35, Application US/09974296
; Patent No. US20020155263A1
; GENERAL INFORMATION:
    TITLE APPLICANT: Chen, Huei-Mei
; TILLE REFRENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                     DB 14;
                                                                                                                                                                                                                                                                     Query Match
15.8%; Score 584.2; DB 14
Best Local Similarity 98.7%; Pred. No. 1.8e-138;
Matches 589; Conservative 0; Mismatches 8;
                LOCATION: (44)...(44)

MAME/KEY: misc_feature

LOCATION: (2456)..(2456)

COTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2468)..(2468)

COTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2468)..(2468)

COTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2511)..(2511)

COTHER INFORMATION: n equals a,t,g, or c

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  NAME/KEY: misc feature
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TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION UNDER:

CURRENT APPLICATION NUMBER:

CURRENT FILING DATE:

2002-03-27

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR PILING DATE:

1999-09-29

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

1999-10-03

PRIOR FILING DATE:

1999-11-03

NUMBER OF SEQ ID NOS:

8654

SOFTWARE:

PARIOR FILING DATE:

1999-11-03

NUMBER OF SEQ ID NOS:

8650

SOFTWARE:

PARIOR TILING DATE:

1999-11-03

NUMBER OF SEQ ID NOS:

1007-11-03

SEQ ID NO 183
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                                                                                     GCTAATTCGCTCTGTTTTGTATTTATGTTGATTTACTAAATTGGGTTCATTATCTTAT
                                                                                                                                                                                                                                                           193 GCTAATTCGCTCTGTTTTTTTATGTTGATTTACTAAATTGGGTTCATTATCTTTTAT
                       0; Gaps
                       Indels
    Pred. No. 1.8e-138;
0; Mismatches 8;
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LOCATION: (12)...(12)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (28)...(28)
OTHER INFORMATION: n equals a,t,g,
98.7%;
Best Local Similarity 98.7 Matches 589; Conservative
                                                              2763 CCAGCAAGCGGAACCT
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ORGANISM: Homo sapiens
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Sequence 1612, Application US/10085783A

Sequence 1612, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

TILE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

FILE REPRENCE: 4231/2002

FILE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

FILE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

FURBRIT FILING DATE: 2002-02-28

FRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn Version 3.2

LENGTH: 541
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llarity 96.2%; Pred. No. 4.1e-117;
Conservative 0; Mismatches 20;
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511; Conserv
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; ORGANISM: Human
US-10-085-783A-16172
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Best Local S
Matches 511
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                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                Indels 217;
                                                                                                                                                                                          Length 2209;
                                                                                                 ) NAME/KEY: misc feature
) OTHER INFORMATION: Incyte ID No. US20020156263A1 022404.23
US-09-974-298-35
                                                                                                                                                                                   Score 546.8; DB 9;
Pred. No. 6.2e-129;
0; Mismatches 7;
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                                                                                                                                                                                     Query Match
Best Local Similarity 78.3%;
Matches 808; Conservative
SEQ ID NO 35
LENGTH: 2209
TYPE: DNA
ORGANISM: Homo mapiens
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